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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent 10 application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of 15 UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_FETAL_LIVER.txt, 25 created 24 January 2001, having 25,630,231 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, Drug Discov. Today
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, Science
280:995 (1998); Pennisi, Science 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of 5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, 10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the 15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many 20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that 25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting 30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et 35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENSCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., 5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic 10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily 20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach 25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from 30 cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries 35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 . The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single 10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally 15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, 20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of 25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the 35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified 5 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon 10 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a 15 plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at 20 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. 30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said 15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

20 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more 25 preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

30 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention, 25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 12,673 or a complementary sequence or a 30 fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a 35 nucleotide sequence as set out in any of SEQ ID NOS.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring 5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe 10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous 15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, 25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or 30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first 35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, 5 said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is 10 provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

15 measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said 20 exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ 25 ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

30 In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from 35 the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,130 - 37,156, or fragment 5 thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display 10 can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound 20 collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase 25 "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1) (suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and 30 Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably 35 disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences 5 that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS... The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, 10 are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF 15 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a 20 nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another 25 with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and 30 biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are 35 capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

15 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

20 FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

30 FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or 35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one
5 tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression
10 (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or
15 that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30}) ("known");
20

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

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FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and
35 then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting inter alia of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher 5 eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that 10 are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of 15 regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a 25 given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for 30 experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in 35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in 5 process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can 10 be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a 15 combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation 20 can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the 25 like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an 30 experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly 35 to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene 15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding 20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences 25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be 30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements 35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate 5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any 15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given 25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated 30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are 35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods 5 and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the 10 presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that 15 newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery 20 can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, 25 depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by 30 process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

35 When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".
5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, or regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although 5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be 10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as 15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated 20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene 25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be 35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative 5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

15 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

20 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

25 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene- 30 specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using 5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance 10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested 15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for 20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred 25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention 30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of 35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by 5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture 10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying 15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the 20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can 25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or 30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from 5 somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and 10 Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed 15 consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential 20 expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high 25 stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon 30 quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are 35 well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of 5 discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For 10 purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide 15 redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by 20 deposition of mRNA-derived nucleic acids, (2).those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized 25 probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., 30 or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

35 Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus,
5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved
10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of
15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used
20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA.

Typically, at least about 50, 60, 70, 80 or 90% of the
30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides
35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the 5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* 10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 - 5% – have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome 25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as 35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above-described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets,
10 hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions 5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of 10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first 15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the 20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of 25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of 30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable 35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - 5 can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 10 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the 15 record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored 20 locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at 25 which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present 30 invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being 35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence 5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the 10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored 15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of 20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user 25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or 30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene 35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be 20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among 25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of 30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as 5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including 10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right 15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of 20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing 25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using 30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during 35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.

15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode 5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in 10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray 20 hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently 25 available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of 30 human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health 35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and 5 iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, 10 and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing 15 damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

20 During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but 25 provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

30 As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV 35 glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 5 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy 10 findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The 15 hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitch et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between 20 ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, Science 236:410-416 (1987), defined 25 two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both 30 men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and 35 antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL), low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation). Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., Arterioscler. Thromb. Vasc. Biol. 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., Am. J. Hum. Genet. 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., *Nature Genet.* 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., *Am. J. Hum. Genet.* 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary sclerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., *New Eng. J. Med.* 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform 10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually 15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary 25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with 30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen 35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrom 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents,

10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following

15 Schistosoma mansoni infection.

The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have genetic bases or contributions.

Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single 5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression 15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for 25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single 30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of 35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and 5 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for 20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., 35

"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell 5 Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol. 46(3):425-8 (1999)), in drug discovery screens (see, for 10 example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer 15 Progression," Cancer Res. 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in 20 expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is 25 evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead 30 compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the 35 relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements 5 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity 15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA 20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes 25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a 30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known 35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are 5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form 10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

15 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' 25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present 30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived 35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a 5 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that 10 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable 15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention 20 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 – 25,129, respectively, for probe SEQ ID NOS. 1 – 12,673. The minimum amount of ORF required to be 25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 – 25,129 individually by routine experimentation using standard high stringency 30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl 35 poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; 5 Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment 10 and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis 15 (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention 20 to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 25 can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
5 that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
10 program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb
5 window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification,
10 as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-
15 modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per
20 gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique
25 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences
30 also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the
35 universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, 5 but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with 10 hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression 15 ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which 20 were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average 25 hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

30 One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA 35 (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 15 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2Gene Expression Measurements From Genome-Derived Single
5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series 10 of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message 15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial 20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II 30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. 35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution 5 containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics 15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference 20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, 25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when 30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is 35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all 5 tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue 10 or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class 15 (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of 20 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative 25 expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results 30 returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant 35 homology (white: E values < 1e-100; gray: E values from 1e-

05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (Origene Technologies,
35

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present 5 in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

10 Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the 15 observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes 20 from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

25 For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, 30 approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

35 Table 2

**Function of the Most Highly
Expressed Genes Expressed Only in Brain**

Microarray Sequence Name	Normal Signal	Expressed Ratio	Homology to EST	Gene Function as described by GenBank in GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191
15 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α_1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be 10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical 15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification 20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the 30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the
5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

20 The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

25 Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

30 The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be 5 useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) 10 query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as 20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective 25 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of 30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is 35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: . The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1×10^{-5}) and 1e-100 (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 12,673) and probe exon (SEQ ID NOS.: 12,674 - 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid
5 probes as claimed in any of claims 1 to 7, wherein at least
50% of said single exon nucleic acid probes lack
prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid
10 probes as claimed in any of claims 1 to 8, wherein at least
50% of said single- exon nucleic acid probes lack
homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in any of claims 1 - 9 characterised in
that said set of probes is addressably disposed upon a
substrate.

11. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in claim 10 wherein said substrate is
selected from glass, amorphous silicon, crystalline silicon
and plastic.

12. A microarray comprising a spatially addressable set of
25 single exon nucleic acid probes as claimed in any of claims
1 - 11.

13. A single exon nucleic acid probe for measuring human
gene expression in a sample derived from human Fetal liver
30 comprising a nucleotide sequence as set out in any of SEQ
ID NOs.: 1 - 12,673 or a complementary sequence or a
fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid molecule expressed in the
human Fetal liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any 10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

25 18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
475	13108	256800	4.41				
822	13535	260333	9.9				
1083	136888		2.9				
1345	13940	28462	10.32				
1658	14248	28792	2.58				
1678	14270	268633	5.03				
1763	14353	268898	1.73				
1785	14375	26819	0.88				
1782	14382	26827	9.24				
1935	14519	27075	1.21				
2021	14603	27198	3.24				
2210	14788	27900	4.38				
2318	14880	27445	2.04				
2607	15169	27735	0.88				
2807	15168	27738	0.88				
3220	15832	28311	1.65				
3498	16101	28578	1.22				
3589	16170	28832	10.28				
3617	16220		0.8				
3719	16319	28797	0.97				
4020	16818		0.94				
4275	16881	28310	1.53				
4349	16935	28378	8.4				
4388	16955	28398	0.74				
4389	16955	28397	0.74				
4430	17016		1.3				
4962	17537	28979	1.04				
5007	17580		0.59				
5054	17827	30071	0.81				
5187	17762	30197	5.85				
5212	17777	30198	1.32				
5462	18097	30415	2.1				
5462	18097	30416	2.1				
5615	18244		5.84				

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Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408			9.03			
5859	18244			4.85			
5910	18532	31257	0.84				
5915	18537	31262	3.16				
6173	24759	31552	1.41				
6200	18810	31579	1.65				
6548	19146		1.28				
6868	18284	32087	1				
6868	18284	32088	1				
7178	19711	32559	1.13				
7179	19711	32560	1.13				
7441	18986	32831	1.4				
7441	18985	32832	1.4				
8005	20547	33451	1.65				
8422	20982	33878	1.45				
8794	21333	34257	0.57				
8794	21333	34258	0.57				
9453	21978	34931	4.84				
9681	22180	35155	0.78				
9796	22294	35277	1.19				
9858	22431	35408	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10226	22820	35815	0.65				
10326	22920	35816	0.65				
10563	23098		3.08				
10725	24798	36268	2.48				
10908	23425		2.99				
11238	23789	36827	2.73				
11338	23034	36043	1.87				
11338	23034	36044	1.87				
11934	23826		2.69				
12117	24370		2.19				
12439	24570	30814	1.8				

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	18813	31533	14.37	9.8E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 16, 18, 17 and 18
7949	20490	33400	1.85	9.8E+00	U327116.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9858	22157	35128	0.47	9.8E+00	Y18930.1	NT	Sulfobabesia sofitanicus 281 kb genomic DNA fragment, strain P2
9858	22157	35129	0.47	9.8E+00	Y18930.1	NT	Sulfobabesia sofitanicus 281 kb genomic DNA fragment, strain P2
7073	18845	32483	0.8	9.8E+00	AF085689.1	NT	Calulus galus ornithine transcarbamoylase (OTC) gene, exon 1
7073	18845	32494	0.8	9.8E+00	AF085689.1	NT	Calulus galus ornithine transcarbamoylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.6E+00	AF242432.1	NT	Mus musculus Nafp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nrip1) and general transcription factor IIIH polypeptide 2 (Grf2h2) genes, complete cds
10319	22813	35809	1.22	9.6E+00	AF242432.1	NT	Mus musculus Nafp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nrip1) and general transcription factor IIIH polypeptide 2 (Grf2h2) genes, complete cds
2889	15247	27814	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (pM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	15247	27815	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (pM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2850	15566	28040	3.19	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8042	20584	33491	0.88	9.3E+00	AF130880.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8833	21471	34390	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1(IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP39)
5500	18134	30543	2.82	9.1E+00	AF085689.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5500	18134	30544	2.82	9.1E+00	AF085689.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21885		0.9	9.0E+00	P08241	SWISSPROT	RHODOPSIN
6188	18786	31584	5.12	8.9E+00	BE971808.1	EST_HUMAN	6016510388R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:38945923'
6517	18117	31807	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTox3 premature mRNA, partial cds
6517	18117	31908	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTox3 premature mRNA, partial cds
465	13098	25580	1.66	8.4E+00	5031804	NT	Homo sapiens Insulin receptor substrate 1 (IRS1) mRNA
8376	20315	33217	3.8	8.1E+00	AJ31719.1	NT	Zea mays mRNA for legumain-like protease (sec2a)
11048	23561		2.47	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8092	20833		0.76	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7384	18910		1.95	7.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8302	20843	33784	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33785	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5998	18869	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:42855085'
8888	21227	34147	2.63	7.4E+00	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4
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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
								Top Hit	Database Source
8683	21227	34148	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		
3006	15622	28096	3.19	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds		
3006	15622	28100	3.19	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds		
7097	18668	32507	0.7	7.2E+00	BE178080.1	EST HUMAN	RCO-H170813-200308-031-007 H170813 Homo sapiens cDNA		
7203	19734	32585	1.22	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)		
7203	19734	32586	1.22	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)		
9516	22016					NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91		
11283	23791	36848	3.2	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 kDa PROTEIN IN MRDA-PHPB INTERGENIC REGION		
8882	22389	35357	3.35	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)		
11129	23937	36679	1.87	7.0E+00	O22489	SWISSPROT	WD-40 REPEAT PROTEIN L4 (L2)		
8225	20768	33684	4.06	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)		
10253	22748	35736	1.2	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS		
7849	20391	33253	1.38	6.8E+00	W03412.1	EST HUMAN	zab7c11.11 Saccharomyces cerevisiae 2B18H Homo sapiens cDNA clone IMAGE:281860_5'		
7849	20391	33294	1.38	6.8E+00	W03412.1	EST HUMAN	zab7c11.11 Saccharomyces cerevisiae 2B18H Homo sapiens cDNA clone IMAGE:281860_6'		
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP6]		
8080	21597				1.13	6.8E+00	P38307	SWISSPROT	
10110	22805	35595	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 167.0 kDa PROTEIN C38C10.5 IN CHROMOSOME III		
5488	18122				0.69	6.6E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
8888	22481	35485	1.89	6.6E+00	Q92E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDYL MONOPHOSPHATE KINASE) (UMP KINASE)		
8888	22481	35468	1.89	6.6E+00	Q82E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDYL MONOPHOSPHATE KINASE) (UMP KINASE)		
11008	23522				2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C863.05C
9108	21644	34584	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP30]		
10208	22701	35895	0.49	6.5E+00	BEB86001.1	EST HUMAN	60167843SF1 NIH_3T3 Homo sapiens cDNA clone IMAGE:3980989_5'		
9857	22156	35127	1.11	6.2E+00	A7010901.1	NT	Schizosaccharomyces pombe unknown mRNA		
10455	22849	35958	0.53	6.2E+00	6754621	NT	Mus musculus mannose-2, alpha B1 (Man2b1), mRNA		
7102	19872	32511	1.34	6.0E+00	BE780163.1	EST HUMAN	601468031TF1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303_5'		
9730	22228	31205	0.46	6.0E+00	AP000098.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 11680001-1485000 nt. position (8/7)		
10407	22801	35898	0.6	6.0E+00	AE001882.1	NT	Deltacoccus radiodurans R1 section 1 of 2 of the complete chromosome 2		
10407	22801	35897	0.6	6.0E+00	AE001882.1	NT	Deltacoccus radiodurans R1 section 1 of 2 of the complete chromosome 2		
							Mus musculus misspelled lineage kinase 3 (Mll3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds		
6843	19239	32042	6.67	5.8E+00	AF155142.1	NT	Homo sapiens DESC1 protein (DESC1), mRNA		
3576	16180				1.18	5.8E+00	7881557	NT	
7215	19748	32801			0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19746	32802			0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	20087			1.31	5.6E+00	P75080	SWISSPROT DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11349	23047	36059		2.68	5.6E+00	Q55276	SWISSPROT LYCOPENE BETA CYCLASE
63389	18002	31790		0.73	5.5E+00	P47447	SWISSPROT HEAT-INDUCTIBLE TRANSCRIPTION REPRESSOR HRCA
10658	23180			1.54	5.5E+00	AF175425.1	NT <i>Mus musculus</i> DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23048	36058		3.79	5.5E+00	P11880	SWISSPROT PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024			2.08	5.5E+00	AL181671.2	NT, <i>Anabidopsisthaisana</i> DNA chitosanase 4, coding fragment No. 67
7009	18507	32328		1.2	5.4E+00	X022212.1	NT <i>Chicken alpha-cardiac actin</i> gene
7009	18507	32327		1.2	5.4E+00	X022212.1	NT <i>Chicken alpha-cardiac actin</i> gene
7389	18895			0.72	6.4E+00	Q98436	SWISSPROT NEI PROTEIN PRECURSOR (NEI-RELATED PROTEIN 2)
7811	20354			1.58	5.4E+00	Q91082	SWISSPROT VITELLOGENIN PRECURSOR (VTP) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8734	21273	34193		0.78	5.4E+00	P40378	SWISSPROT REP1 PROTEIN
8734	21273	34194		0.78	5.4E+00	P40379	SWISSPROT REP1 PROTEIN
9949	22444	35423		1.33	5.4E+00	Q17084	SWISSPROT RHODOPSIN
9949	22444	35424		1.33	5.4E+00	Q17084	SWISSPROT RHODOPSIN
4889	17474	28890		1.52	5.3E+00	L43128.1	NT <i>Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds</i>
6814	18211			0.67	5.3E+00	P41778	SWISSPROT HOMEBOX PROTEIN CEH-20
8024	20568			3.71	5.3E+00	P54098	SWISSPROT DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8914	21452			0.62	5.3E+00	AB0324990.1	NT <i>Homo sapiens</i> HERPUD1 gene for stress protein Herp, complete cds
9655	18282			1.04	5.2E+00	BE184840.1	EST_HUMAN QVA-HT0681-270400-188-f09 HT0681 <i>Homo sapiens</i> cDNA
10274	22769			0.78	5.2E+00	AF248870.1	NT <i>Drosophila orientalis</i> R1B retrotransposon element reverse transcriptase gene, partial cds
11074	23596			2.1	5.2E+00	Q10138	SWISSPROT HYPOTHETICAL 61.1 KD PROTEIN C23E2.08C IN CHROMOSOME 1
8892	21430	34354		0.88	5.1E+00	O18005	SWISSPROT RHODOPSIN
9739	22237	35217		0.87	5.1E+00	P09182	SWISSPROT COLICIN N IMMUNITY PROTEIN (MICROCOLIN N IMMUNITY PROTEIN)
6430	18033	31817		0.85	5.0E+00	BF310443.1	EST_HUMAN 601884910F1 NIH_MGC_19 <i>Homo sapiens</i> cDNA clone IMAGE:4124114 5'
10086	22591			0.69	5.0E+00	BF308561.1	EST_HUMAN 601880420F1 NIH_MGC_17 <i>Homo sapiens</i> cDNA clone IMAGE:4131508 5'
10327	22821	35817		3.37	5.0E+00	AF1622445.2	NT <i>Canis familiaris</i> skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11170	23877	38723		13.54	5.0E+00	Z83880.1	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10131	22826			0.71	4.9E+00	U91228.1	NT Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4135	16727			12.06	4.8E+00	AF185255.1	NT <i>Eunice australis</i> histone H3 (H3) gene, partial cds
8095	20838	33547		0.65	4.8E+00	BF307809.1	EST_HUMAN RC3-GN0042-100800-011-c10 GRK042 <i>Homo sapiens</i> cDNA
8478	21017			4.96	4.8E+00	AW750087.1	EST_HUMAN PM0-BT0547-310100-002-b04 BT0547 <i>Homo sapiens</i> cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3111	12886	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3112	12886	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3312	15923	28399	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C380
9124	21659	34601	1.09	4.6E+00	BE848437.1	EST_HUMAN	7688910X1 NCI_CGAP_Clu_1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140
9124	21659	34602	1.09	4.6E+00	BE848437.1	EST_HUMAN	7688910X1 NCI_CGAP_Clu_1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140
10280	22785		0.77	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11474	23824	36894	1.98	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11598	24039	37108	1.67	4.5E+00	BF868841.1	EST_HUMAN	60212328F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4289716 5'
3078	15891	28164	1.53	4.4E+00	BF530893.1	EST_HUMAN	60207255F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3078	15891	28165	1.53	4.4E+00	BF530893.1	EST_HUMAN	60207255F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4215284 5'
6349	18854		1.8	4.4E+00	X13414.1	NT	Murine 1 gene for MHC class II(a) associated invariant chain
6288	18874		0.82	4.3E+00	AF058679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7484	19898	32851	2.38	4.3E+00	Y13402.1	NT	Plasmidium falciparum R289R+var1 gene, exon 1
7911	20124	33001	0.84	4.3E+00	AE001222.1	NT	Tropoena pallidum section 38 of 87 of the complete genome
10741	23268	36282	8.92	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
							MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE)
5708	18334		3.21	4.2E+00	P10444	SWISSPROT (RDP)	
5780	18405	31121	1.46	4.2E+00	PS1828	SWISSPROT LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)	
68889	19803	32435	1.88	4.2E+00	P13983	SWISSPROT EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
68889	19803	32438	1.88	4.2E+00	P13983	SWISSPROT EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
88890	21428	34953	4.85	4.2E+00	AI808013.1	EST_HUMAN wif3_93_xrl Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23806892 3'	
98332	22330	35912	2.07	4.2E+00	P31388	SWISSPROT NUBBIN PROTEIN (TWAIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)	
7168	19898	32545	0.81	4.1E+00	BE253668.1	EST_HUMAN 601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'	
7284	19792	32648	1.7	4.1E+00	BP247389.1	EST_HUMAN 601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089758 5'	
7657	20169	33058	8.1	4.1E+00	O23810	SWISSPROT YY1 PROTEIN PRECURSOR	
7759	20297	33163	4.03	4.1E+00	P28884	SWISSPROT GENE 68 PROTEIN	
7759	20297	33164	4.03	4.1E+00	P28884	SWISSPROT GENE 68 PROTEIN	
7857	20399	33308	2.78	4.1E+00	U57503.1	NT Pan troglodytes novel repetitive solo LTR element in the RNU2 locus	
9459	21985	34898	0.63	4.1E+00	P11253	SWISSPROT 50S RIBOSOMAL PROTEIN L4	
9590	22090	35034	2.26	4.1E+00	BF892425.1	EST_HUMAN 602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333208 5'	

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
102038	22703		0.5	4.1E+00	P48414	SWISSPROT	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
104899	22893	36003	0.62	4.1E+00	Q84242	SWISSPROT	HYPOTHETICAL PROTEIN HMLF1
10765	23289		2.97	4.1E+00	P08716	SWISSPROT	EST_HUMAN 601507510F1 NIH_3T3 cDNA clone IMAGE:300890315
10851	23372		13.84	4.1E+00	BE885880.1	SWISSPROT	GLC7-INTERACTING PROTEIN 1
35889	16203		0.82	4.0E+00	P38229	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
58550	18615	32336	0.74	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
58550	18616	32337	0.74	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	18615	32336	0.85	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	18615	32337	0.85	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7240	19769	32825	1.34	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22585	35560	0.6	4.0E+00	AE002132.1	NT	Unpublished ureayticum section 33 of 59 of the complete genome
10158	22853	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10158	22853	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23874	36937	3.99	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
35550	16154	28833	4.79	3.9E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23874	36933	3.99	4.0E+00	P07584	NT	N.tabacum chitinase gene 50 for class I chitinase C
4413	18698		0.74	3.9E+00	AF055468.1	NT	Mus musculus seminal vesicle secretory protein B9 (MSVSP88) gene, promoter region (HLA-H1) gene, RoR α gene, and sodium phosphate transporter (NPT3) gene, complete cds
58339	18463	31186	3.08	3.9E+00	BE814357.1	EST_HUMAN	MFR-BN0070-300500-028-H05 BN0070 Heme sapiens cDNA
58339	18463	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MFR-BN0070-300500-028-H05 BN0070 Heme sapiens cDNA
6746	18339	32145	0.71	3.9E+00	AF268209.1	NT	Dicytostelium discoideum non-LTR retrotransposon TREB-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6792	18693	32188	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H1) gene, RoR α gene, and sodium phosphate transporter (NPT3) gene, complete cds
6855	18532	32357	4.12	3.8E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7398	18623	32787	6.09	3.6E+00	M23807.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8259	20800	33718	2.15	3.8E+00	X658865.1	NT	Xleavis mRNA for M4 muscarinic receptor
11269	23007	36014	3.27	3.8E+00	Y18000.1	NT	Human sepius NF2 gene
11291	23743	36800	1.62	3.8E+00	AA861489.1	EST_HUMAN	nr18e12 s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gba1A0416 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN)
2858	15217		1.1	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J89 section 123 of 132 of the complete genome
6525	19125	31918	0.78	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8371	20811	33831	1.06	3.8E+00	D44725.1	EST_HUMAN	HUMSUPHY35 Human brain cDNA Homo sapiens cDNA clone 148
9710	22208		0.55	3.8E+00	AJ380981.1	NT	Streptococcus oralis partial apt gene for xanthine phosphoribosyltransferase, strain NCTC7894
4092	16887	28144	13.58	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7218	19749		0.79	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8842	21181		0.53	3.7E+00	4503950	NT	Human sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9105	21641	34581	0.68	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11308	23801	36861	3.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36862	3.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
11767	24158		1.28	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
6119	13248	25719	2.6	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS_Homo sapiens cDNA clone MD5BUE10 6'
49117	17492		0.99	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21026	33942	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8487	21026	33943	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8579	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8579	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10733	22269					NT	Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gpdE), the translation start site has been verified (gpdG), and repressor protein (gprR) genes, complete cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6151	18784		1.08	3.5E+00	L42888.1	NT	Bacillus burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6360	18984	31742	0.92	3.5E+00	R19745.1	EST_HUMAN	yg40cc08.11 Soares Infant brain 1NI8 Homo sapiens cDNA clone IMAGE:34940 5'
8421	20981		0.55	3.5E+00	P24657	SWISSPROT	THROMBOXANE-A-SYNTHASE (TXA SYNTHASE) (TXS)
8882	21500	34421	0.88	3.5E+00	AA180988.1	EST_HUMAN	zp88b04.s1 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element :
8982	21500	34422	0.88	3.5E+00	AA180988.1	EST_HUMAN	zp88b04.s1 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element :
9414	21923	34872	1.12	3.5E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1559	14151	26883	4.49	3.4E+00	AF254577.1	NT	Brassica napus RP8-6 mRNA, complete cds
2612	15174	27742	1.02	3.4E+00	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7397	18822	32786	2.85	3.4E+00	PO4052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7680	20189	33086	0.88	3.4E+00	PO4052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8811	21150		0.89	3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8003	21540	34470	0.7	3.4E+00	AJ228042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8040	21577	34508	0.5	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for latrapsin protein, exon 6
10165	22880	35685	3.61	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11408	23857	36822	1.93	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6218	18828	31601	0.9	3.3E+00	Q048689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q048689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7834	20378	33281	0.88	3.3E+00	AF11198.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10381	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10381	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
5228	13168	26840	1.72	3.2E+00	X084422.1	NT	D.virio 2p-50 POU gene
4088	13158	25840	0.7	3.2E+00	X084422.1	NT	D.virio 2p-50 POU gene
4836	17413	28886	1.24	3.2E+00	4502404	NT	Homo sapiens carboxylic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31065	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31068	1.24	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	19049	31634	1.88	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	19049	31835	1.88	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7801	20114	32891	0.84	3.2E+00	PO4276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7750	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf1, ycf3, rps18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf1, ycf3, rps18 genes
8980	21488		4.84	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NFE] HYDROGENASE SMALL SUBUNIT (NFE HYDROGENASE SMALL CHAIN)
8449	21975	34927	1.52	3.2E+00	M36383.1	NT	S.cerevisiae mitochondrial deaminase (ILV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	AB016081.2	NT	Oryza sativa latifolia OIGC2 gene for guanylyl cyclase C, complete cds
11727	24133		4.08	3.2E+00	L38383.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6035	18654	31398	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 1426 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7421	18645	32810	0.97	3.1E+00	PS2178	SWISSPROT	TRIOSE PHOSPHATE PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7711	20220			1.09	3.1E+00 AF303225.1	NT	Bacillus clausophilus peptidyl hydrolase (pepE) gene, complete cds
8538	21077	33995		4.27	3.1E+00 P48894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
8538	21077	33998		4.27	3.1E+00 P48894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
9183	21780			3.77	3.1E+00 Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMNDAR2C)
9249	21775	34726		0.52	3.1E+00 Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22308	35292		0.75	3.1E+00 7524759	NT	Chlorella vulgaris chloroplast, complete genome
9889	22398			0.58	3.1E+00 Q10125	SWISSPROT	HYPOTHETICAL 56.3 kD PROTEIN F52C9.5 IN CHROMOSOME III DEOXYHYDROSYNTHASE (DHS)
10239	22734	35726		4.7	3.1E+00 P48285	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11338	23036			2.91	3.1E+00 P33315	SWISSPROT	retinoic acid nuclear receptor isoform beta 2 [mouse, embryonal carcinoma cell line, PC37-MZ1, mRNA, 2871 nt]
11355	23809			7.48	3.1E+00 S56860.1	NT	
12490	24619			1.38	3.1E+00 U77668.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds
18541	18173	30588		1.68	3.0E+00 X53098.1	NT	Saureus genes encoding Saurell DNA methyltransferase and Saurell restriction endonuclease
6873	18269	32073		0.72	3.0E+00 X56037.1	NT	Corynebacterium glutamicum frtC gene for threonine synthase (EC 4.2.88.2)
6873	18269	32074		0.72	3.0E+00 X56037.1	NT	Corynebacterium glutamicum frtC gene for threonine synthase (EC 4.2.88.2)
7209	18740			10.44	3.0E+00 P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH461)
7247	18776			0.77	3.0E+00 Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
88838	21377			1.33	3.0E+00 X67838.1	NT	B. napus DNA for myrosinase
10195	22890	35883		0.53	3.0E+00 Q58805	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10527	23094	36073		1.62	3.0E+00 Q16161	SWISSPROT	CD10 PROTEIN HOMOLOG
10888	23409	36428		7.04	3.0E+00 P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GCF)
10888	23409	36427		7.04	3.0E+00 P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GCF)
2055	14638	27207		2.32	2.9E+00 AE002225.2	NT	Chlamydomonas pneumoniae AF259, section 53 of 94 of the complete genome
6224	18833			0.88	2.9E+00 AB026033.1	NT	Bonopeltis pedata mitochondrial DNA for 16S ribosomal RNA
6889	19487	32309		3.74	2.8E+00 Z36878.1	NT	Fringilla galapagoensis P-protein of the glycine cleavage system
7262	19790	32844		4.37	2.8E+00 O14514	SWISSPROT	BRAIN-SPECIFIC ANGIogenesis INHIBITOR 1 PRECURSOR

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	19780	32845	4.37	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7479	20001	32888	6.04	2.8E+00	P48589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
							STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
7809	20352	33200	0.87	2.8E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
7809	20352	33201	0.87	2.8E+00	P05844	SWISSPROT	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20583	33460	0.89	2.8E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Bm84_Homo sapiens cDNA clone IMAGE:4153058 5'
1504	14088	28634	4.87	2.8E+00	AF186398.1	NT	<i>Budus harlandii</i> matrasse K (matk) gene, partial cds; chloroplast product
1675	14287		3.45	2.8E+00	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 52
7348	19874	32740	4.88	2.8E+00	8393724	NT	<i>Mus musculus</i> endomucin (LOC53423), mRNA
9531	22031		0.57	2.8E+00	BE865182.1	EST_HUMAN	60134275SF1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3684807 5'
10569	19874	32740	1.68	2.8E+00	8393724	NT	<i>Mus musculus</i> endomucin (LOC53423), mRNA
251	12811	26364	9.31	2.7E+00	68768306	NT	<i>Mus musculus</i> per-heptamer repeat gene 3 (Phox3), mRNA
251	12811	25395	9.31	2.7E+00	68768306	NT	<i>Mus musculus</i> per-heptamer repeat gene 3 (Phox3), mRNA
5740	18368	31073	1.2	2.7E+00	L140035.1	NT	Homo sapiens apolipoprotein Kringle IV gene, exons 1 and 2
6088	20828		0.8	2.7E+00	U15947.1	NT	Ipnomea purpurea chalcone synthase (CHS8) gene including complete 5'UTR and complete cds
8898	21436		1.68	2.7E+00	AL118459.1	NT	Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9353	20282	33101	0.83	2.7E+00	AW088191.1	EST_HUMAN	XP88612X1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10394	22888		1.48	2.7E+00	BE083527.1	EST_HUMAN	CNA-8T0281-031180-087-404 B10281 Homo sapiens cDNA
4781	17382	28812	4.97	2.6E+00	AF098749.1	NT	<i>Mus musculus</i> sphingomyelin kinase (SPHK1b) mRNA, complete cds
6738	18382	31088	1.94	2.6E+00	67556801	NT	<i>Mus musculus</i> SRY-box containing gene 13 (Saxt13), mRNA
5736	18382	31089	1.94	2.6E+00	67556801	NT	<i>Mus musculus</i> SRY-box containing gene 13 (Saxt13), mRNA
5882	18812		2.42	2.6E+00	Y17062.1	NT	Myobacterium fortuitum furA II gene
7689	20188		5.98	2.6E+00	AF235602.1	NT	<i>Mus musculus</i> Sh2-containing inositol 5-phosphatase (Ship) gene, exons 18 through 27, and complete cds
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptani EV1-83
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptani EV1-83
8579	22076	35038	3.02	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 40
10257	22752		1.51	2.6E+00	9055193	NT	<i>Mus musculus</i> cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
10807	23423	38443	1.69	2.6E+00	AF143675.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
12390	24888		2.78	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	26840	2.29	2.5E+00	AJ271184.1	NT	<i>Aspergillus nidulans</i> neQ gene for DNA helicase, exons 1-4
1513	14105	26841	2.29	2.5E+00	AJ271184.1	NT	<i>Aspergillus nidulans</i> neQ gene for DNA helicase, exons 1-4

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Descriptor
59881	18601	31334	1.71	2.5E+00	P13485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
59881	18601	31335	1.71	2.5E+00	P13485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
65585	18601	31334	1.39	2.5E+00	P13485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
65585	18601	31335	1.39	2.5E+00	P13485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
88228	19418	32234	0.73	2.5E+00	D30052.1	NT	Vibrio cholerae cbA gene and cbB gene for cholera toxins, complete cds	
7738	20244	33135	1.05	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-2015-077 FT0005 Homo sapiens cDNA	
90322	21569	34468	1.75	2.5E+00	D50307.1	NT	Rice DNA for addicase C-1, complete cds	
97688	22284	35247	0.88	2.5E+00	BE297758.1	EST_HUMAN	601175778F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'	
11724	24131		1.68	2.5E+00	AF289885.1	NT	Mus musculus Elavl4H gene, partial cds; LMK1 gene, complete cds; and ELN gene, partial cds	
3047	15683	28144	0.9	2.4E+00	I242822.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end	
50533	17807	30052	6.78	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA	
61611	18774	31536	4.02	2.4E+00	P02843	SWISSPROT	VITELLOGENINI PRECURSOR (YOLK PROTEIN 1)	
8082	20624	33536	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)	
8082	20624	33537	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)	
8153	20694		2.33	2.4E+00	AE001488.1	NT	Helicobacter pylori, strain J98 section 47 of 132 of the complete genome	
8585	21124		1.62	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-C31289-01-405 P1004 Homo sapiens cDNA	
8762	21301	34222	8.16	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)	
9851	22446	35427	2.59	2.4E+00	P13473	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR	
9851	22446	35428	2.59	2.4E+00	P13473	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR	
10017	22612	35504	1.62	2.4E+00	X02511.1	NT	H.sapiens CTGF gene and promoter region	
10141	22838		7.38	2.4E+00	P09090	SWISSPROT	XYLOOSE KINASE (XYLUOKINASE)	
10225	22720	36710	1.63	2.4E+00	BE328702.1	EST_HUMAN	hr6306_x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'	
10225	22720	35711	1.63	2.4E+00	BE328702.1	EST_HUMAN	hr6306_x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'	
10483	22877	35988	1.27	2.4E+00	O51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ	
108958	23473	36498	1.68	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosome DNA, region 75 degrees: dppPFK operon and downstream	
11237	23768	36826	2.27	2.4E+00	AF158852.2	NT		
1238	13880	26413	11.15	2.3E+00	Z46724.1	NT	Fragaria x ananassa cytochrome c oxidase parviflorae (ApxSC) gene, ApxSC-c allele, complete cds	
4189	16788		1.65	2.3E+00	AJ401081.1	NT	Gdomesticus artificial single chain antibody gene (L3)	
60000	18620		0.91	2.3E+00	N88245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYCARBOXYPEPTIDASE	
7477	18889	32884	2.54	2.3E+00	6978854	NT	Rattus norvegicus ATPase, Cat++ transporting, ubiquitous (Atp2a3), mRNA	
7593	25120		4.61	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	
7756	20264	33159	1.08	2.3E+00	X60286.1	NT	M.macosae drak and dral genes homologues coding for Drak and Dral	

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8038	21575	34505	0.53	2.3E+00	5835317	NT	Polymerase alpha/polymerase mitochondrial, complete genome
8087	21633	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE-3'-L-FUCOSYLTRANSFERASE)
10681	23213	36224	2	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FLUT-IV)
11612	24055	37119	2.92	2.3E+00	BF541887.1	EST_HUMAN	ANXIN VII (SYNEVIN)
11612	24055	37120	2.82	2.3E+00	BF541887.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4008173 5'
11850	24278	31020	7.31	2.3E+00	BE885237.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4008173 5'
4089	16885	28143	91.07	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4403	16888	28432	4.5	2.2E+00	D67071.1	NT	Putative gene for regucalcin, exon1 (non-coding exon)
4403	16888	28433	4.5	2.2E+00	D67071.1	NT	Put gene for regucalcin, exon1 (non-coding exon)
5545	18177	30591	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDR) RELATIVE WITH 11 LIGAND-BINDING REPEATS (LR1) />
5545	18177	30592	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDR) RELATIVE WITH 11 LIGAND-BINDING REPEATS (LR1) />
6016	18635	31373	0.85	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-808 CT0254 Homo sapiens cDNA
6016	18635	31374	0.85	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-808 CT0254 Homo sapiens cDNA
6212	18822	31593	9.1	2.2E+00	BE250368.1	EST_HUMAN	600813401771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6495	18098	31880	4.32	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6709	18303	32197	3.04	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SONATOMEDIN A)
7037	18057		3.58	2.2E+00	AA594574.1	EST_HUMAN	605602.81 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058378 3'
7358	19884	32747	0.9	2.2E+00	AA157027.1	EST_HUMAN	2187704.71 Strategene fetal retina 8372022 Homo sapiens cDNA clone IMAGE:568143 5'
7602	20115	32892	25.23	2.2E+00	AA448012.1	EST_HUMAN	205510.71 Scaree_total_fetus_Nz21-Fg_9w Homo sapiens cDNA clone IMAGE:785634 5'
8048	20588	33494	0.65	2.2E+00	BE301580.1	EST_HUMAN	bb17m12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D468338 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8048	20588	33495	0.65	2.2E+00	BE301580.1	EST_HUMAN	bb17m12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D468338 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9265	21791		12.17	2.2E+00	BE741078.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
8488	24783		2.57	2.2E+00	Q04708	SWISSPROT	TRANSPOSON TY1 PROTEIN A
8868	22481	35443	1.96	2.2E+00	A1290373.1	EST_HUMAN	qm58b03.x1 Scaree_placenta_8deweeks_2NHP866W Homo sapiens cDNA clone IMAGE:1883865 3' similar to gb:T00433 GLUTATHIONE PEROXIDASE (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
98888	22461	35444	1.98	2.2E+00	AI290373.1	EST_HUMAN	qmr69b03_x1 Scores _placenta_Biotrueks_2NbHP869W Homo sapiens cDNA clone IMAGE:1883985 3'
10008	22503	35494	3.7	2.2E+00	BF248782.1	EST_HUMAN	similar to qb:y00433 GLUTATHIONE PEROXIDASE (HUMAN); 601855591FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	22847	35841	2.99	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 (Ode protein hGR74 homolog mRNA, complete cds)
11316	23014	36023	4.01	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11482	23932	37003	4.23	2.2E+00	P10407	SWISSPROT	EARLY E/T 28 KD PROTEIN
585	15419	25639	6.28	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region IMAGE:2734550 3'
3848	16251	3848	0.85	2.1E+00	AW449368.1	EST_HUMAN	UH-B13-44kV-e-08-0-J11 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:270618 3'
6281	18889	32471	0.85	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG3022 HOMOLOG
68888	18033	32471	3.38	2.1E+00	O70159	SWISSPROT	ALPHA-2 HS-GLYCOPROTEIN PRECURSOR (FETUINA)
							yy08a10.31 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to qb:M55654
7110	19450	32288	5.13	2.1E+00	N28575.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM20008871 5'
10454	22848		0.58	2.1E+00	Y10284.1	NT	H.sapiens TRAF1 gene, putative promoter region
1238	13838	28352	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dok1 (DOKDEL) mRNA, complete cds
1238	13836	28353	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dok1 (DOKDEL) mRNA, complete cds
1380	13873	28501	0.82	2.0E+00	AF204927.1	NT	Oncoblegus carinatus Nef_K+-ATPase beta 1 subunit mRNA, complete cds
1619	14212		2.89	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2194	14770	27343	3.69	2.0E+00	Z78278.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2194	14770	27344	3.69	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4176	16767	28215	1.9	2.0E+00	AW864498.1	EST_HUMAN	H1305.X1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:2872168 3' similar to qb:X01677
4176	16767	28216	1.9	2.0E+00	AW864498.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); H1305.X1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:2872168 3' similar to qb:X01677
7552	20071		0.77	2.0E+00	P07588	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7887	20509	33415	3.98	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
7887	20509	33416	3.58	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
7887	20509	33417	3.88	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
88533	21392	34314	3.82	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
122295	24946	308522	7.77	2.0E+00	5834843	NT	Celius galus mitochondrion, complete genome
5784	18409	31124	6.89	1.8E+00	6754389	NT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
5784	18409	31125	6.89	1.8E+00	6754388	NT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
6249	18859	31630	1.2	1.8E+00	BIE888895.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'

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8780	19353			1.02	1.8E+00 AWB46689.1	EST_HUMAN	MRO-CT00683-071089-002-002 CT00683 Homo sapiens cDNA
6845	19435			2.31	1.8E+00 Q83627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8398	20838	33888		2.16	1.8E+00 P02487	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
8398	20838	33888		2.16	1.8E+00 P02487	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
8593	21132			2.45	1.8E+00 BF360208.1	EST_HUMAN	CN2-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8825	21384			1.35	1.8E+00 Q51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
8648	22048	35009		0.8	1.8E+00 AA689125.1	EST_HUMAN	ab9-ne04_31 Strategene lung (R937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains AU repetitive element contains element L1 L1 repetitive element;
10458	22850	35989		0.52	1.8E+00 AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3128	15742	28211		1.88	1.8E+00 P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3154	15768	28224		2.42	1.8E+00 U04358.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15768	28235		2.42	1.8E+00 U04358.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6027	18648			2.02	1.8E+00 P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6253	18862	31624		2.02	1.8E+00 BF311969.1	EST_HUMAN	601887854f1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4127384 5'
6532	18132			1.53	1.8E+00 BF683327.1	EST_HUMAN	602139470f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4288272 5'
6838	18428	32244		1.35	1.8E+00 BF3058632.1	EST_HUMAN	6018834488f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	18459	32274		1.08	1.8E+00 P21249	SWISSPROT	MAJOR ANTIGEN
8060	20602	33512		0.81	1.8E+00 P11368	SWISSPROT	RETRON/VIUS-RELATED POL-POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8060	20602	33513		0.81	1.8E+00 P11369	SWISSPROT	RETRON/VIUS-RELATED POL-POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8788	21327	34252		2.12	1.8E+00 O43281	SWISSPROT	EMBRYONAL FN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577		0.63	1.8E+00 R31042.1	EST_HUMAN	YH72638.1f1 Soares placenta Nb2H4P Homo sapiens cDNA clone IMAGE:135278 5'
9108	21703	34845		0.8	1.8E+00 AW88004.1	EST_HUMAN	Q9P-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
9763	22281	35244		0.87	1.8E+00 P27050	SWISSPROT	CHITINASE D PRECURSOR
10163	22678			3.78	1.8E+00 AF111848.1	NT	Homo sapiens PR00530 mRNA, complete cds
10447	22841			0.85	1.8E+00 P44326	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12075	24915			6.85	1.8E+00 AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12163	24403			4.98	1.8E+00 9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Actc1b), mRNA
12476	24815	30790		1.38	1.8E+00 BF212412.1	EST_HUMAN	601813714f1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'

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1147	13750	28258	2.08	1.7E+00	Q80114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)	
2311	14883	27458	2.37	1.7E+00	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080	
2411	14979	27554	1.29	1.7E+00	AI141087.1	EST_HUMAN	c243n05.x1 Scroes_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'	
4558	17141	28590	0.74	1.7E+00	Q80114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)	
5787	18422	31137	1.65	1.7E+00	BE033548.1	EST_HUMAN	CM0-BT0282-171289-127-05 BT0282 Homo sapiens cDNA	
5787	18422	31138	1.65	1.7E+00	BE033548.1	EST_HUMAN	CM0-BT0282-171289-127-05 BT0282 Homo sapiens cDNA	
6168	18780	31545	3.35	1.7E+00	Q81178	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)	
7270	18788	32654	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 kD PROTEIN IN CAT2AMD1 INTERGENIC REGION	
7270	18788	32655	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 kD PROTEIN IN CAT2AMD1 INTERGENIC REGION	
7306	19834	32693	1.63	1.7E+00	P20383	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)	
7786	20339	33247	0.98	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters	
7978	20518	33425	1.34	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA	
8006	20548	33452	0.57	1.7E+00	BF530830.1	EST_HUMAN	602071917F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214689 5'	
8479	21018	33833	0.61	1.7E+00	AF245513.1	NT	Hippocampus Hippocampus Interferon inducible hbx protein (Hbx) mRNA, complete cds	
8562	21101	34001	2.08	1.7E+00	BF369000.1	EST_HUMAN	6011894265F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'	
8838	21177	34088	0.49	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid erytroph	
8838	21177	34097	0.49	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid erytroph	
9078	24792	34545	2.25	1.7E+00	O80479	SWISSPROT	HOMEBOX PROTEIN DLX-3	
9078	24792	34548	2.25	1.7E+00	O80479	SWISSPROT	HOMEBOX PROTEIN DLX-3	
9524	22024		1.85	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds	
11467	23917	36985	2.18	1.7E+00	W2242.4	EST_HUMAN	6787 Human retina cDNA Tsp509I cleaved sublibrary Homo sapiens cDNA clone IMAGE:2267549 3' similar to contains MSR1.11 tu82307.1N1 NCI CGAP_Gaa4 Homo sapiens cDNA clone IMAGE:2267549 3' similar to contains MSR1.11	
12030	24320	30953	1.52	1.7E+00	AI678443.1	EST_HUMAN	MSR1 repetitive element;	
12558	24659	30873	1.79	1.7E+00	AI198573.1	EST_HUMAN	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds	
2078	14858	27229	21.82	1.6E+00	AF198339.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds	
2087	14688	27238	4.3	1.6E+00	AF077374.1	NT	Mus musculus ST6GalNAcII gene, exon 2	
2083	14673	27243	1.04	1.6E+00	Y11344.1	NT	Mus musculus gene encoding endo-polysaccharidase	
2323	14684		1.13	1.6E+00	X98373.1	NT	B.laevis gene encoding endo-polysaccharidase	
2388	15804	28084	1.5	1.6E+00	W58428.1	EST_HUMAN	ZD23805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN); gb:D23805	
- 4104	18888		7.23	1.6E+00	Bf570077.1	EST_HUMAN	gb:D23805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN); gb:D23805	

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4444	17030	29470	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4444	17030	29471	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
							Urobilin chinenensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5145	17715	30145	0.9	1.6E+00	AF075384.4	NT	Urobilin chinenensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
6145	17715	30148	0.8	1.6E+00	AF075384.4	NT	Urobilin chinenensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus STO609a/cili gene, exon 2
5243	17807	30229	2.2	1.6E+00	Y11344.1	NT	Mus musculus STO609a/cili gene, exon 2
5993	18813	31347	1.95	1.6E+00	LD4808.1	NT	Brachydonto rufi NHC class II DA-beta-2701 gene, 3' end
6072	18889	31434	0.92	1.6E+00	AF005681.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6596	18193	31688	0.93	1.6E+00	BF280703.1	EST_HUMAN	IL2-UT0073-060690-145-E02 UT0073 Homo sapiens cDNA IMAGE:Z727511.3'
6811	18402	32218	1.07	1.6E+00	AW24881.1	EST_HUMAN	U1-H-B12-ehr-b-04-0-ULs1 NCI CGAP Sub4 Homo sapiens cDNA
7283	18821	32680	2.32	1.6E+00	BE897287.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7873	20515		1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MV/HOMOLOG
8320	20861	33798	3.24	1.6E+00	AJ2877131.1	NT	Mus musculus SII_MAP_17_CYP_a_SCL & CYP_b genes
8831	21370	34294	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8831	21370	34295	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9381	24790	33221	3.16	1.6E+00	X562046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
8381	24780	33222	3.16	1.6E+00	X562046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
8649	22148	35119	1.34	1.6E+00	T41280.1	EST_HUMAN	ph568_1991TV Outward Alu-primed hcdNA library Homo sapiens cDNA clone ph568_1991TV
10052	22547	35541	0.52	1.6E+00	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine/threonine kinase 1 (AK1), and zinc finger protein (DNZ1) genes, complete cds
10088	22583	35575	0.92	1.6E+00	AW835684.1	EST_HUMAN	QV4-LT0018-0802020-100-d07 LT0016 Homo sapiens cDNA
10088	22583	35576	0.92	1.6E+00	AW835684.1	EST_HUMAN	QV4-LT0018-0802020-100-d07 LT0016 Homo sapiens cDNA
10248	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23182	36198	1.58	1.6E+00	PS4817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN]
10686	23216	36228	1.58	1.6E+00	PS4817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN]
							Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
10723	18889	31434	8.41	1.6E+00	AF005681.1	NT	Homo sapiens unknown mRNA
11552	24000	37072	2.92	1.6E+00	AF104313.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
35	12714	25173	4.02	1.5E+00	U53449.1	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
252	12812	25398	2.17	1.5E+00	AE0022012	NT	
649	13272		1.98	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metangridin) (Adam15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1930	14544	27101	2.55	1.5E+00	AF275285.1	NT	Mus musculus receptor protein tyrosine phosphatase- <i>rho</i> (P _Y nt) gene, exons 10 and 11 and partial cds
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato Virus A RNA complete genome, isolate U
2558	15120	27690	1.83	1.5E+00	88778350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.54	1.5E+00	AJ131402.1	NT	Potato Virus A RNA complete genome, isolate U
3421	16028	28510	0.7	1.5E+00	AE001945.1	NT	Deltaproteobacter radiobacter R1 section 82 of 228 of the complete chromosome 1
8803	18525	31250	0.84	1.5E+00	AI855301.1	EST_HUMAN	h1_2110_x1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.;
8803	18525	31251	0.94	1.5E+00	AI855301.1	EST_HUMAN	h1_2110_x1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.;
6538	19137	31630	2.68	1.5E+00	R17878.1	EST_HUMAN	y910e02_r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31683 5'
7182	19714		1.37	1.5E+00	BE785358.1	EST_HUMAN	601478745f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32568	20.84	1.5E+00	P47170	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7214	19745	32800	20.84	1.5E+00	P47178	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	18908	32774	1.02	1.5E+00	AA889259.1	EST_HUMAN	ak28f10_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8065	20807	33510	0.85	1.5E+00	BE887448.1	EST_HUMAN	601508958bf1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8578	21117	34031	1.1	1.5E+00	K02138.1	NT	Mouse gamma IgM chain gene, mu-delta region
8948	21484		0.53	1.5E+00	AB039518.1	NT	Homo sapiens IgG1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9061	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	601882602f1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085135 5'
9404	21913	34862	0.9	1.5E+00	R81928.1	EST_HUMAN	y632h01_r1 Soares placenta Nb2h1P Homo sapiens cDNA clone IMAGE:1417697 5'
9553	22053	35016	1.12	1.5E+00	AW375397.1	EST_HUMAN	QV3-CT0192-281089-008-009 CT0192 Homo sapiens cDNA
9774	22272	35257	5.97	1.5E+00	BF378754.1	EST_HUMAN	RC0-TN0078-150800-034-905 TN0078 Homo sapiens cDNA
8865	22460		1.47	1.5E+00	BF337944.1	EST_HUMAN	60203577f1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183885 5'
10583	22583	35565	2.85	1.5E+00	AA017889.1	EST_HUMAN	2638g08_r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:3813065 5'
10583	22583	35583	2.85	1.5E+00	AA017889.1	EST_HUMAN	2638g08_r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:3813065 5'
11277	23730	36785	4.1	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 s1 547 (synonym: hfr1) Homo sapiens cDNA clone DKKZp547P243 3'
11416	23867		8.57	1.5E+00	X07390.1	NT	Mouse mitochondrial tRNA-Ser gene and tRNA-Phs pseudogene
12022	25010	30615	1.59	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12255	24465		4.99	1.5E+00	AL445085.1	NT	Thermoplasma ectophillum complete genome; segment 3/3
32	12711	25169	1.8	1.4E+00	7881685	NT	Homo sapiens DKFZp588m0122 protein (DKFZp588m0122), mRNA
32	12711	25170	1.8	1.4E+00	7881685	NT	Homo sapiens DKFZp588m0122 protein (DKFZp588m0122), mRNA
1774	14384	28809	1.32	1.4E+00	H19856.1	EST_HUMAN	ym576c3_r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:172540 5'
2316	14888		0.88	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2372	14942		7.8	1.4E+00	U67822.1	NT	Ovis aries prion protein gene, complete cds

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
26833	15250	27820	1.45	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
28022	15354	27822	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAV protein (BAW), and WS81 protein (WS81) genes, complete cds
28022	15354	27823	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAV protein (BAW), and WS81 protein (WS81) genes, complete cds
3378	15885		0.88	1.4E+00	5453733	NT	Human papillomavirus type 7 genomic DNA
4342	16929	28369	1.14	1.4E+00	AW80456.1	EST_HUMAN	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAV protein (BAW), and WS81 protein (WS81) genes, complete cds
4342	16929	28370	1.14	1.4E+00	AW80455.1	EST_HUMAN	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAV protein (BAW), and WS81 protein (WS81) genes, complete cds
4685	17267		1.78	1.4E+00	BF881547.1	EST_HUMAN	00215688771 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297558 5'
5575	18208	30657	1.78	1.4E+00	AW054978.1	EST_HUMAN	00215688771 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297558 5'
5719	18345		5.04	1.4E+00	AB032863.1	NT	Human sapiens mRNA for KIAA1157 protein, partial cds
6425	18028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	26116		4.4	1.4E+00	AB020712.1	NT	Human sapiens mRNA for KIAA0805 protein, complete cds
6544	18143	31838	2.32	1.4E+00	Q8Z777	SWISSPROT	SYNAPSIN II
8544	19143	31937	2.32	1.4E+00	Q8Z777	SWISSPROT	SYNAPSIN II
6583	19181	31881	0.67	1.4E+00	11086333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6911	18570	32398	0.77	1.4E+00	AW883057.1	EST_HUMAN	CA2-NN0008-30300-132-b12 NN0008 Homo sapiens cDNA
7330	19857	32720	2.31	1.4E+00	AJ13289.1	NT	Human sapiens canesin-1/2 locus, Contig 1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7343	19870	32735	1.1	1.4E+00	AW46770.1	EST_HUMAN	IMAGE:2918873 3' similar to contains AU
8277	20818		0.88	1.4E+00	P07683	SWISSPROT	GLUCOSAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8728	21268		4.01	1.4E+00	AJ271795.1	NT	Human sapiens Yq pseudautosomal region, segment 1/2 repetitive element
8023	21560	34487	2.13	1.4E+00	R20459.1	EST_HUMAN	Yg33f12.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'
9125	21680	34683	3.72	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301288-012-f05 BT0313 Homo sapiens cDNA
9158	21683	34637	0.58	1.4E+00	AF334844.1	NT	Sceloporus undulatus, ornithine transcarbamylase (OTC) mRNA, complete cds
10109	22804	35694	0.77	1.4E+00	BF575545.1	EST_HUMAN	602133135f1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10150	22845	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281088-008-C04 HT0188 Homo sapiens cDNA
10150	22845	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281088-008-C04 HT0188 Homo sapiens cDNA
10418	22912	35812	1.11	1.4E+00	D83441.1	NT	Pandora columbianae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10418	22912	35813	1.11	1.4E+00	D83441.1	NT	Pandora columbianae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10848	23463	36435	2.16	1.4E+00	AA185528.1	EST_HUMAN	ZF8600.1 Scores_NHNM/Pu_S1 Homo sapiens cDNA clone IMAGE:685512 5' similar to contains element MER22 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23614	36854	6.28	1.4E+00	AB006882.1	NT	Homo sapiens APCECED mRNA for AIRE-1, complete cds
11283	23736	36791	3.92	1.4E+00	BE862107.2	EST_HUMAN	601653184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23735	36792	3.92	1.4E+00	BE862107.2	EST_HUMAN	601653184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	36855	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
11304	23797	36856	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
11885	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12287	25108		2.38	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen set0-2 (SE70-2), mRNA
598	13225		1.38	1.3E+00	Z73840.1	NT	M.mucedo gene encoding 4-Dihydromethyl-Hisopropate dehydrogenase
925	13548	26085	2.33	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1168	13770		22.19	1.3E+00	Y19213.1	NT	Homo sapiens putative psoriasis pseudogene for hair keratin, exons 2 to 7
1340	13935	28456	13.87	1.3E+00	4507888	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1340	13935	28457	13.87	1.3E+00	4507888	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1400	13894		1.05	1.3E+00	U81730.2	NT	Coxi lacrimate-faci diphodiolinates synthetase (dapaA) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)
2586	15149		0.97	1.3E+00	BE868735.2	EST_HUMAN	and MASP-related protein, complete cds
2968	15581	28060	0.68	1.3E+00	6755821	NT	601681233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3857	16260	28732	0.81	1.3E+00	AF016894.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
4713	15581	28060	1.31	1.3E+00	6755821	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kDa erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete >
5184	17749	30178	0.82	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30179	0.82	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18531		1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
6169	18781		7.47	1.3E+00	AW352834.1	EST_HUMAN	PM0-CT0288-291198-004-f08 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW352834.1	EST_HUMAN	PM0-CT0288-291198-004-f08 CT0289 Homo sapiens cDNA
6549	19147	31943	1.24	1.3E+00	M33498.1	NT	D.melanogaster no-alpha transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00158	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6926	19595	32415	0.85	1.3E+00	MI3818.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7033	19597	32394	1.01	1.3E+00	BE5338818.1	EST_HUMAN	601681420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447985 5'

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
7157	18889	32633	0.79	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0569 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Hamo sapiens cDNA clone TCBAP0569
7481	20003	32698	3.97	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
82239	20790	33701	2.06	1.3E+00	AJ008812.1	NT	Sus scrofa pip gene
83894	20924	33844	2.54	1.3E+00	BE583379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38661185 3'
84986	21035	33956	0.89	1.3E+00	BE574290.1	EST_HUMAN	601680250R2 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3950532 3'
8844	21182		1.57	1.3E+00	BB10247	NT	Homo sapiens GL004 protein (GL004), mRNA
87253	21284	34184	0.88	1.3E+00	AI027629.1	EST_HUMAN	w085607_x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2462100 3'
90773	21610	34540	0.48	1.3E+00	HA2881.1	EST_HUMAN	y088603_s1 Soares breast 3NIBI8s1 Homo sapiens cDNA clone IMAGE:183078 3'
90773	21610	34541	0.48	1.3E+00	HA2881.1	EST_HUMAN	y088603_s1 Soares breast 3NIBI8s1 Homo sapiens cDNA clone IMAGE:183078 3'
9434	21880		4.54	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21889	34917	2.12	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for photolysis
9443	21889	34918	2.12	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for photolysis
8642	22042	35003	1.1	1.3E+00	AF059250.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
95288	22088	35002	1.62	1.3E+00	O08754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
96695	22184	35137	1.21	1.3E+00	AI027628.1	EST_HUMAN	w085607_x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2462100 3'
97440	22238	35218	0.83	1.3E+00	AJ223982.1	NT	Lactobacillus lactis cremoris NCDO-Ly1 chromosomal inversion junction DNA
97440	22238	35219	0.83	1.3E+00	AJ223982.1	NT	Lactobacillus lactis cremoris NCDO-Ly1 chromosomal inversion junction DNA
9780	22278	35283	3.85	1.3E+00	BE583378.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38661185 3'
10114	22809	35600	1.25	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 48 of 83 of the complete chromosome
10130	22825	35815	2.41	1.3E+00	M28853.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970		0.65	1.3E+00	AI183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22888		0.52	1.3E+00	BB10247	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008	0.48	1.3E+00	HA2881.1	EST_HUMAN	y088603_s1 Soares breast 3NIBI8s1 Homo sapiens cDNA clone IMAGE:183078 3'
10507	23001	36009	0.48	1.3E+00	HA2881.1	EST_HUMAN	y088603_s1 Soares breast 3NIBI8s1 Homo sapiens cDNA clone IMAGE:183078 3'
10573	23108		4.66	1.3E+00	Q14117	SWISSPROT	DIHYDROPRIMIDINASE (DHPS) (HYDANTOINASE) (DHP)
10785	23309	36316	2.3	1.3E+00	P252389	SWISSPROT	mRNA 3'-END PROCESSING PROTEIN RNAs
10807	23330	36342	2.17	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
111216	23718		1.87	1.3E+00	AW274781.1	EST_HUMAN	xp088603_x1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2739868 3'
11414	23885	36928	3.09	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007	3.09	1.3E+00	Z886882.1	NT	Bacillus subtilis genomic DNA 23.6kB fragment
12011	24312		3.63	1.3E+00	AF187873.1	NT	Carica papaya inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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12182	24473	30949		3.47	1.3E+00 BF348043.1	EST_HUMAN	802023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156452 5'
12204	24828			1.78	1.3E+00 P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24500			2.08	1.3E+00 AF187035.1	NT	Stomatilium cytochrome b gene, complete cds; mitochondrial product
12873	24904			1.25	1.3E+00 AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
678	13302	25784		9.75	1.2E+00 AA678246.1	EST_HUMAN	222608.81 Soares_fetal_fibr_spleen_cDNA clone IMAGE:431535 3'
858	13472	25983		1.04	1.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHPR-III)
858	13472	25984		1.04	1.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHPR-III)
858	13472	25985		1.04	1.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHPR-III)
911	13524			1.9	1.2E+00 882234	NT	Homo sapiens hypothetical protein PRCC077 (PRCC077), mRNA
1203	13803	28316		4.87	1.2E+00 AF080245.2	NT	Eleutherodactylus coqui tenease mRNA, complete cds
1247	13844	28381		1.3	1.2E+00 AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	28382		1.3	1.2E+00 AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14635	27208		53.59	1.2E+00 AF140831.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14985	27559		1.53	1.2E+00 AF152495.1	NT	Homo sapiens post-synaptic density 35 (DLG4) gene, complete cds
3144	15758	28224		1.18	1.2E+00 AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287		7.17	1.2E+00 AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3201	15813	28288		7.17	1.2E+00 AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3325	15835			3.43	1.2E+00 P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3389	18007	28446		0.57	1.2E+00 AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3774	18374	28839		8.66	1.2E+00 U75802.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4058	18655	28121		1.87	1.2E+00 BF373570.1	EST_HUMAN	MR0-F10175-050800-203-p08_1_F10175_Homo sapiens cDNA
4386	18007	28448		1.12	1.2E+00 AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4570	17153			2.09	1.2E+00 M87000.1	NT	Rattus norvegicus AE3 gene, exons 1-23
4621	17204	28953		1.08	1.2E+00 AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4658	17241	28955		1.5	1.2E+00 AF158485.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4680	17272			9.41	1.2E+00 Y08200.1	NT	T_phinnatum chloroplast rbcL gene, partial
4791	18008			0.77	1.2E+00 M81778.1	NT	G_gallus T-cadherin mRNA, complete cds
56229	18258	30729		1.06	1.2E+00 U20760.1	NT	Human enterocellular calcium-sensing receptor mRNA, complete cds
5743	18398	31077		2.27	1.2E+00 AW813276.1	EST_HUMAN	MF23-S10197-140200-013-c05 S10191 Homo sapiens cDNA
6034	18853	31395		0.72	1.2E+00 AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6300	18908	31679		2.17	1.2E+00 X74885.1	NT	D_hydei ey1 repeat cluster DNA, fragment D
6361	18865	31743		3.98	1.2E+00 BE003113.1	EST_HUMAN	QV4-BN0080-270400-180-e03 BN0080 Homo sapiens cDNA
6423	18036	31822		1.43	1.2E+00 X88084.1	NT	C_glutamicum per gene and scaA gene
6433	18036	31823		1.43	1.2E+00 X88084.1	NT	C_glutamicum per gene and scaA gene

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8475	19078	31858	34.98	1.2E+00	AA758254.1	EST_HUMAN	ab4q12.s1 Scores testis_NHT Homo sapiens cDNA clone 1322274 3'
66289	19226	32030	2.26	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0181-140200-013-c05 ST0181 Homo sapiens cDNA
68885	19493	32314	1.18	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	18505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828		0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 112
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cDNA Homo sapiens cDNA clone cdNAFH03 5'
7848	20158	33045	2.84	1.2E+00	X74207.1	NT	Lactis pyrD and pyrF genes
8504	21043	33884	3.05	1.2E+00	AB033380.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLYL TRANSFERASE)
8597	21138	34051	0.89	1.2E+00	P38427	SWISSPROT	
8809	21348		0.53	1.2E+00	7708271	NT	Homo sapiens CGI-30 protein (LOC51811). mRNA
8855	21463	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA
8319	21833	34783	2.92	1.2E+00	Z32850.1	NT	R communis gene for pyrophosphate-dependent phosphofuctokinase beta subunit
8523	22023	34881	1.86	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone fhm01a01
9844	22342	35324	3.47	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific endopeptidase
10220	22724		0.87	1.2E+00	AB0098688.1	NT	Homo sapiens klotho gene, exon 1
11224	23765	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0284-161189-001-d01 ST0284 Homo sapiens cDNA
11252	23790		0.84	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-q10 HT0422 Homo sapiens cDNA
11331	23209	36038	3.73	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11878	24907	30712	32.4	1.2E+00	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C003
11888	24304		2.11	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
4889	13122	25888	1.19	1.1E+00	D86880.1	NT	Human mRNA for KIAA0227 gene, partial cds
1788	14389	28624	1.49	1.1E+00	AW885983.1	EST_HUMAN	QV0-BN0042-170300-163-912 BN0042 Homo sapiens cDNA
2817	15179	27748	1.09	1.1E+00	AF087124.1	NT	Wheat yellow mosaic virus RNA 1/70 kDa precursor protein gene, complete cds
3373	15981	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
35533	16133	28620	0.84	1.1E+00	89226841	NT	Homo sapiens hypothetical protein RJ10749 (FLJ10749). mRNA
3639	16242	28718	1.08	1.1E+00	AB052860.1	EST_HUMAN	wf5h11_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW_P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;
3781	16381	28845	1.41	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 228 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 228 of the complete genome
3889	16488		0.81	1.1E+00	X853774.1	NT	H.paranaemolaeus hifilm(A), hifilm(C), hiflr and menB genes
4016	16614	29037	0.67	1.1E+00	89226841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749). mRNA

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exn ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4083 16888	28145	0.65	1.1E+00	6755205	NT	<i>Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pemb7), mRNA</i>
4285 16881		7.81	1.1E+00	5685331	NT	R.unicolor complete mitochondrial genome
5131 17703	30137	3.54	1.1E+00	U18486.1	NT	African swine fever virus, complete genome
5132 17704	30138	0.86	1.1E+00	AJ271740.1	NT	<i>Drosophila melanogaster D-Titin gene, exons 1-37</i>
5201 17768	30180	1	1.1E+00	U34740.1	NT	<i>Emarginata nitidula stargomatoxystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcG), (stcL), (stcM), (stcN), (stcO), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds</i>
5230 17794	30213	0.86	1.1E+00	X78425.1	NT	<i>E.faecalis pop5 gene</i>
5409 17988		.1.04	1.1E+00	AE003869.1	NT	<i>Xylella fastidiosa, section 15 of 228 of the complete genome</i>
5510 18143	30555	1.52	1.1E+00	6878530	NT	<i>Rattus norvegicus Aquaporin 4 (Aqp4), mRNA</i>
5798 18423	31139	19.88	1.1E+00	BE980184.1	EST_HUMAN	<i>60165277R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'</i>
5915 18439	31161	3.23	1.1E+00	AII38582.1	EST_HUMAN	<i>qd85c03.x1 Scarens tests_NHT Homo sapiens cDNA clone IMAGE:1738260 3'</i>
6242 18851	31621	1.25	1.1E+00	11419739	NT	<i>Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA</i>
6420 19023	31807	0.71	1.1E+00	AF197881.1	NT	<i>Macroglossum pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product</i>
6539 19138	31931	0.71	1.1E+00	RO8037.1	EST_HUMAN	<i>ye9903.11 Scarens fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1249245</i>
6817 19408	32225	0.7	1.1E+00	AJ40404.1	NT	<i>Mus musculus mRNA for ER protein 58 (EP58 gene)</i>
7338 19885	32729	0.78	1.1E+00	X56881.1	NT	<i>Meiozo mRNA for endope (2-phospho-D-glycerate hydrolase)</i>
7501 20023	32986	2.08	1.1E+00	Z72338.1	NT	<i>Herpes simplex virus type 1 (strain KOS) UL41 gene</i>
7501 20023	32987	2.08	1.1E+00	Z72338.1	NT	<i>Herpes simplex virus type 1 (strain KOS) UL41 gene</i>
7521 20041	32910	8.72	1.1E+00	AL161598.2	NT	<i>Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84</i>
7580 24787	32973	0.86	1.1E+00	11867900	NT	<i>Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Str2), mRNA</i>
8074 20616	33530	2.8	1.1E+00	BF083896.1	EST_HUMAN	<i>60208258EF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:42468285</i>
8163 20704	33620	0.76	1.1E+00	AI478339.1	EST_HUMAN	<i>Im38H11.31 NCI_CGAP_Kid11 Homo sapiens mRNA for stretch responsive muscle (X-chromosome) protein (Smox gene)</i>
8672 21211	34130	0.75	1.1E+00	AB003088.1	NT	<i>Acetabularia caliculus mitochondrial COX1-like gene</i>
8749 21268	34208	0.78	1.1E+00	S90750.1	NT	<i>Vh=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]</i>
8858 20297		0.68	1.1E+00	BE584876.1	EST_HUMAN	<i>6012782770F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:38174185</i>
8946 22046	35007	0.68	1.1E+00	AJ245772.1	NT	<i>Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smox gene)</i>
9590 22099		0.81	1.1E+00	Y12227.1	NT	<i>Arabidopsis thaliana DNA, 24 kb surrounding PFL locus</i>
9687 22183	35160	0.84	1.1E+00	L78301.1	NT	<i>Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds</i>

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9747	22245	35226	1.59	1.1E+00	AB023151.1	NT	Human sepius mRNA for KIAA0934 protein, partial cds
9850	22348	35330	4.82	1.1E+00	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 27
8809	22408	35381	19.39	1.1E+00	67564021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22889	35883	1	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23087	36079	2.83	1.1E+00	11087384	NT	Human sepius KIAA0828 gene product (KIAA0828), mRNA
10586	23121		4.06	1.1E+00	AF068942.1	NT	Klobosomium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
10978	18028		5.28	1.1E+00	6822873	NT	mitochondrial protein, partial cds
10983	23497	38528	3.76	1.1E+00	AF012882.1	NT	Human sepius hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	38527	3.76	1.1E+00	AF012882.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1), mRNA, complete cds
11234	23785	38822	6.02	1.1E+00	AI803898.1	EST HUMAN	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1), mRNA, complete cds
11846	24275		1.82	1.1E+00	P07806	SWISSPROT	W78611_Xt1_Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2381548_3'
12051	24335	30987	2.25	1.1E+00	AF216898.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12184	24803		1.64	1.1E+00	AF24169.1	NT	Tasenia sodium immunogenic protein Ts70 mRNA, partial cds
103	12779		3.22	1.0E+00	U23808.1	NT	Dicystostelium discoideum isoperentmyl pyrophosphate isomerase (Dipi) mRNA, complete cds
118	12780	25271	3.48	1.0E+00	D88425.1	NT	Xenopus laevis rhodopsin gene, complete cds
443	13078		2.14	1.0E+00	AB021684.1	NT	Cavia cobaya mRNA for sarco(endo)plasmic reticulum kinase, complete cds
602	13231	25704	1.53	1.0E+00	AJ251680.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA and 28S rRNA
705	13328	25813	7.12	1.0E+00	AL183218.2	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
707	13328		0.89	1.0E+00	AF125984.1	NT	Haemobaphus erythroleucis chromosome 21 segment HS21(C018
1429	15441		1.73	1.0E+00	X80416.1	NT	Aedes vexans (Meigen) muscle-like protein MuC1 mRNA, complete cds
					V.cartari Algal-CAM mRNA		V.cartari Algal-CAM mRNA
1784	14894	28929	0.91	1.0E+00	AB006531.1	NT	Platiria stali intestinal virus RNA for nonstructured polyprotein, capsid protein precursor, complete cds
2526	15680	27682	1.2	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B
2526	15680	27683	1.2	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B
2800	15517	27886	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2800	15517	27987	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2804	15610		0.83	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3232	15844	28324	0.91	1.0E+00	AA628453.1	EST_HUMAN	af23808_51 Soares_total_fetus_Nb2HF8_SW Homo sapiens cDNA clone IMAGE:1032830_3' similar to WP:CA2D8.3 CE04204 contains element MER22 MER22 repetitive element;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	16730	28189	1.5	1.0E+00	AF222391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4362	16949		0.84	1.0E+00	8822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		1.72	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17900		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB038022.1	NT	Oncorhynchus mykiss srl1 mRNA for rhombosine binding lectin STL1, complete cds
5486	18120	30527	2.58	1.0E+00	297022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6013	18833	31388	4.54	1.0E+00	AF248054.1	NT	Bos taurus microtuber calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18833	31389	4.54	1.0E+00	AF248054.1	NT	Bos taurus microtuber calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6111	18727	31480	1.22	1.0E+00	287341.2	NT	Anabidopsis thaliana DNA chromosome 4, ESSA I FCA coding fragment No. 6
6263	18871	31641	4.41	1.0E+00	PO4501	SWISSPROT	FIBER PROTEIN
6269	18977	31645	1.96	1.0E+00	AW452782.1	EST_HUMAN	UH-BI3-abc-d-03-0-U.1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068368 3'
6615	19212	32018	1.79	1.0E+00	UT8802.1	NT	Mus musculus subtilisin-like serine protease LPC (Pc7) gene, exons 1 to 9, partial cds
6682	19258	32062	0.83	1.0E+00	AF104989.1	NT	Homo sapiens cell cycle protein (P2AC4) gene, exons 2 through 5
6742	19338		1.5	1.0E+00	P46503	SWISSPROT	SRB-11 PROTEIN
6874	19898	32442	1.27	1.0E+00	Y11204.1	NT	V.carteri gene encoding valvocardin
7182	19724	32573	1.22	1.0E+00	SE22770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7483	20016		8.58	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14)(B-LYMPHOCYTE CELL ADHESION MOLECULE)
7687	20208	33093	1.38	1.0E+00	AF182531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	sc79008.31 Strategene lung (4837710) Homo sapiens cDNA clone IMAGE:888781 3'
7902	20444	33349	1.49	1.0E+00	BE888287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 6'
7902	20444	33350	1.49	1.0E+00	BE888287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8084	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8281	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8281	20882	33754	2.1	1.0E+00 Q02207			PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20953		0.85	1.0E+00 P51784			UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20987	33902	0.48	1.0E+00 Q9Y5T5			UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8475	24791	33903	0.48	1.0E+00 Q9Y5T5			UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8513	21052	33974	1.06	1.0E+00 U42720.2	NT		
8859	21198	34116	1.07	1.0E+00 M38427.1	NT		
8185	21712	34655	2.05	1.0E+00 BE907582.1	EST HUMAN		Human immunodeficiency virus gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; Vif protein (vif). Vpr protein (vpr). Tat protein (tat). Rev protein (rev). Vpu protein (vpu). Env protein (env), and Nef protein (nef) genes. >
9402	21911	34860	1.34	1.0E+00	67_53428	NT	Mus musculus chloride channel calcium activated 1 (Cica1). mRNA
9402	21911	34861	1.34	1.0E+00	67_53428	NT	Mus musculus chloride channel calcium activated 1 (Cica1). mRNA
9828	22028	34987	2.06	1.0E+00 AV689554.1	EST HUMAN		AV689554 GKC Homo sapiens cDNA clone GK(CCY)A11 5'
9834	22034	34983	1.33	1.0E+00 U44852.1	NT		Xenopus laevis zona pellucida C glycoprotein precursor (Z2PC) mRNA, complete cds
9834	22034	34984	1.33	1.0E+00 U44852.1	NT		Xenopus laevis zona pellucida C glycoprotein precursor (Z2PC) mRNA, complete cds
8767	22285	35248	0.5	1.0E+00 X15486.1	NT		Human Coronavirus gene for membrane protein
9787	22285	35249	0.5	1.0E+00 X15486.1	NT		Human Coronavirus gene for membrane protein
10021	22616	35510	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10021	22616	35511	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10105	22800	35592	0.75	1.0E+00 AI077920.1	EST HUMAN		c915d07_s1 Soares, senescent_fibroblasts_NbSF Homo sapiens cDNA clone IMAGE:1665801 3'
10230	22725	35716	4.17	1.0E+00 AV758825.1	EST HUMAN		A1758825 BM Homo sapiens cDNA clone BMFAWCO4 5'
10372	22886	35859	19.78	1.0E+00 AA004882.1	EST HUMAN		ZB94602.1 Soares, fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:4288908 5'
10372	22886	35860	19.78	1.0E+00 AA004882.1	EST HUMAN		ZB94602.1 Soares, fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:4288908 5'
10404	22888	35883	0.93	1.0E+00 L11910.1	NT		Human retinoblastoma susceptibility gene exons 1-27, complete cds
10853	23374	36393	1.87	1.0E+00 S90825.1	NT		PBR1-pridine-rich protein [frinton 3] [human, genomic, 888 nt]
11587	18120	30527	1.57	1.0E+00 Z97022.1	NT		Hordeum vulgare gene encoding cysteine proteinase
11837	24201		4.85	1.0E+00 P15306			THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410			3.08 1.0E+00	AW978184.1	EST_HUMAN	EST388283 MAGE sequences, MAGN Homo sapiens cDNA
16168	14209	26742	0.97	9.9E-01 AF245455.1	NT	Drosophila melanogaster regulator of G-protein signaling LOCO III mRNA, complete cds	
16168	14209	26743	0.97	9.9E-01 AF245455.1	NT	Drosophila melanogaster regulator of G-protein signaling LOCO III mRNA, complete cds	
2684	152222	27764	1.17	9.9E-01 AL1633202.2	NT	Homo sapiens chromosome 21 segment HS21C102	
3885	18267		0.94	9.9E-01 AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds	
5816	18440	31162	14.59	9.9E-01 P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN	
6029	18848	31369	0.83	9.9E-01 Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1280.5 IN CHROMOSOME II	
9185	21702		1.39	9.9E-01 US66607.1	NT	Lycopersicon esculentum putative MtI copy 1 nernstode-resistance gene	
9474	21873		2.61	9.9E-01 Q28642	SWISSPROT	B2 BRAODYKININ RECEPTOR (BK-2 RECEPTOR)	
10583	23128	38142	1.68	9.9E-01 AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rt8	
549	13180	25658	1.77	9.9E-01 P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL GLUTAMATE SYNTHASE) (AGS) (NAGS)	
2338	14907		0.89	9.9E-01 AJ003108.1	NT	Cellithrix leechus UBE1 gene derived retroposon on the Y chromosome	
2827	15378		2.05	9.9E-01 AF174644.1	NT	Xenopus laevis rec GTPase mRNA, complete cds	
3869	18467	28830	0.95	9.9E-01 Q67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDODEOXYRIBONUCLEASE IV)	
3872	18470	28933	0.61	9.9E-01 BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	
3872	18470	28934	0.61	9.9E-01 BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	
7250	19770	32834	4.86	9.9E-01 AJ302158.1	NT	Enterobacteriaceae sp. JM883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM883	
7250	19779	32835	4.86	9.9E-01 AJ302158.1	NT	Enterobacteriaceae sp. JM883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM883	
7841	20153	33038	1.13	9.9E-01 BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'	
7841	20153	33039	1.13	9.9E-01 BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'	
8853	21182	34110	0.77	9.9E-01 P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)	
10334	22828		0.56	9.9E-01 AA825685.1	EST_HUMAN	cds55d04..s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1371847 3'	
10874	23396	38410	4.86	9.9E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'	
10874	23395	38411	4.86	9.9E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'	
11587	24040	37108	1.78	9.9E-01 AJ680878.1	EST_HUMAN	b42c10..x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2272292 3'	
12058	24241		1.39	9.9E-01 U521112	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUOSP9), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenosulphotolyase protein >	
7212	19743	32597	2.51	9.7E-01 U28718.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 8,10,11,12 and optional segments b, c, d and e, partial cds	
8440	20580	33895	1.7	9.7E-01 AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds	
8446	20586	33891	1.28	9.7E-01 M60544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11048	23562			5.23	9.7E-01	BF511208.1	EST_HUMAN
12859	24723			2.92	9.7E-01	AL114281.1	NT
4531	17115	29559		0.58	9.6E-01	AF197925.1	NT
4531	17115	29550		0.58	9.6E-01	AF197925.1	NT
4557	17140	28598		1.71	9.6E-01	AW789874.1	EST_HUMAN
59228	18550	31276		3.9	9.6E-01	Z70558.1	NT
59228	18550	31277		3.9	9.6E-01	Z70558.1	NT
83331	20872			1.23	9.6E-01	X85275.1	NT
8785	21324	34248		0.47	9.6E-01	L81138.1	NT
9020	21567	34485		0.62	9.6E-01	AF228843.1	NT
10886	23481	38507		1.81	9.6E-01	AF041427.1	NT
11385	23847	38912		5.18	9.6E-01	AV752805.1	EST_HUMAN
11385	23847	38913		5.18	9.6E-01	AV752805.1	EST_HUMAN
11733	24138			2.36	9.6E-01	11421722	NT
12388	24983	30099		2.8	9.6E-01	U91423.1	NT
2515	15079	27851		1.02	9.5E-01	7705591	NT
2891	15248	27817		1.2	9.5E-01	Q02834	SWISSPROT
3850	16448	28909		1.89	9.5E-01	BE002340.1	EST_HUMAN
3850	16448	28910		1.89	9.5E-01	BE002340.1	EST_HUMAN
8831	21469	34397		0.83	9.5E-01	AI180162.1	EST_HUMAN
9034	21571	34500		1.07	9.5E-01	AW88102.1	EST_HUMAN
11123	23631	38874		1.71	9.5E-01	BF218771.1	EST_HUMAN
11328	23024	38633		1.59	9.5E-01	AW282788.1	EST_HUMAN
32235	15847			1.8	9.4E-01	AF165890.1	NT
3254	15898			2.47	9.4E-01	AF080595.1	NT
8789	21338	34265		0.88	9.4E-01	M80724.1	NT
1768	14358			0.95	9.3E-01	AF242282.1	NT
2882	15220	27792		1.09	9.3E-01	BE071172.1	EST_HUMAN
4107	16701	29154		0.92	9.3E-01	M20219.1	NT
4107	16701	29155		0.92	9.3E-01	M20219.1	NT

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Single-Eyan Bimbaa Expressed in English | iver

Probe Seq ID	Exon NC	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top hit of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	
5858	18481	31204	3.69	9.3E-01	LS6180.1	NT	Spooptera frugiperda methyltransferase/indole dehydrogenase mRNA, complete cds	
8011	20553	33498	1.62	9.3E-01	AA847040.1	EST_HUMAN	ce089b03.s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:13853357	
8748	21287		1.13	9.3E-01	AF08981.1	NT	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds	
8887	21408	34330	1.01	9.3E-01	AL181634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34	
12508	24629	30833	1.87	9.3E-01	11440288	NT	Homo sapiens Inositol 1,4,5-triphosphate receptor, type 2 (IPTR2), mRNA	
12515	24634		2	9.3E-01	AF271207.1	NT	Aedes tigrinus putative large subunit ribosomal protein rp34 mRNA, complete cds	
3278	15887	28389	3.89	9.2E-01	BE822702.1	EST_HUMAN	60144133871 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:38161643'	
5004	17577		0.82	9.2E-01	BF128873.1	EST_HUMAN	6018178174F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:40413835'	
5884	18516		1.41	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (SLC30A4), mRNA	
6140	18764	31512	4.4	9.2E-01	BF037588.1	EST_HUMAN	601461153F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:388440815'	
8578	22078	35042	1.31	9.2E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85	
9863	22162	35135	1.15	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA	
10168	22861	35858	3.47	9.2E-01	11430863	NT	Homo sapiens lysosomal arylsulphatase-like protein 1 (LALP1), mRNA	
10314	22808	35800	1.58	9.2E-01	BF580251.1	EST_HUMAN	7058868.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:35782193 similar to SW_NU54_TRYBB	
10523	23063	36074	1.75	9.2E-01	BE583611.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;	
11568	24016	37085	2.27	9.2E-01	BF132402.1	EST_HUMAN	601534843F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:368887145'	
1688	14259	28783	4.88	9.1E-01	T98675.1	EST_HUMAN	6018203121 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:40520185	
2168	14748		2.38	9.1E-01	8922056	NT	ye5210.81 Severe fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:1213683 similar to contains Ali repetitive element	
3239	15851	28331	0.93	9.1E-01	T28418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	
3239	15851	28332	0.83	9.1E-01	T28418.1	EST_HUMAN	AB200038R Infant brain, LUNI array of Dr. M. Soares 1NB Homo sapiens cDNA clone LLAB200385	
6315	18822	31689	1.42	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF16) mRNA, complete cds	
6830	19226	32031	2.82	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN I-3 PRECURSOR (ITI HEAVY CHAIN H3)	
7577	20683	32870	16.95	9.1E-01	AA806523.1	EST_HUMAN	cb71908.s1 NCI CGAP_GCB11 Homo sapiens cDNA clone IMAGE:13388623'	
7719	20227	33115	3.12	9.1E-01	UT2885.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds	
12083	24978		33.14	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	
3241	15853	28335	0.81	9.0E-01	7681825	NT	Homo sapiens DKF2584M24/23 protein (DKF2584M24/23), mRNA	
3401	16010		0.64	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	
4488	17054	29498	1.44	9.0E-01	AF088810.1	NT	Homo sapiens neurechin III-alpha gene, partial cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7424	19948	32814	0.78	9.0E-01	U42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7450	18974		1.84	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds
9271	21787	34746	0.54	9.0E-01	AF098761.1	NT	Danio rerio semaphorin Z1 mRNA, complete cds
9744	22242	35223	0.47	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
5875	18497	31222	2.49	8.8E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete (i.e. putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 h' nolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit)>
6398	18989		1.27	8.9E-01	X089883.1	NT	Rabbit MHC fragment RLA-DF DNA
8152	20693		0.47	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8385	20005	33824	1.04	8.8E-01	AF258867.1	NT	Oithona nana cytochrome-c oxidase subunit I (cox1) gene, partial cds; mitochondrial gene for mitochondrial product
11618	24058	37122	2.69	8.8E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11827	24262		5.33	8.8E-01	AE002188.2	NT	Chlamydia pneumoniae AR39, section 21 of 84 of the complete genome
4840	17222	28678	2.1	8.8E-01	O26350	SWISSPROT	FUTATTE/F420-DEPENDENT NADP REDUCTASE
5578	18207	30658	0.7	8.8E-01	AF310617.1	NT	Pseudorabies virus E4 glycoprotein M gene, complete cds
10880	23475	36500	3.82	8.8E-01	Z28332.1	NT	M. smegmatis (HUB 5-2-4) DNA from plasmid PMA1
11749	25087		2.27	8.8E-01	D80911.1	NT	Synochrocytis sp. PCG8363 complete genome, 13/27, 1578593-1719843
490	13123	25869	1.48	8.7E-01	AF108653.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2446	15013	27595	1.13	8.7E-01	5901983	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2858	15515	27894	5.67	8.7E-01	AA495863.1	EST_HUMAN	mn05f11.51 NCI CGAP_Pt4.1 Homo sapiens cDNA clone IMAGE:1076877
4845	17423	28675	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xenoderm pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	28878	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xenoderm pigmentosum complementation group C (XPC) gene, intron 9
							Pseudomonas aeruginosa lipoxygenase (lop), putative transcriptional regulatory protein OtbR (otbR), ortho-halobenzoate 1,2-dioxigenase beta-ISP protein OtbB (otbB), and put>
5151	17721		3.08	8.7E-01	AF121970.1	NT	dioxigenase alpha-ISP protein OtbB (otbB), and put>
7883	20525	33431	0.68	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-1-20500-013-007 NN0057 Homo sapiens cDNA
8860	21398	34322	0.75	8.7E-01	AI239456.1	EST_HUMAN	ch38e06_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1849788 3'
8860	21398	34323	0.75	8.7E-01	AI239458.1	EST_HUMAN	ch38e06_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1849788 3'
9853	22152	35122	1.7	8.7E-01	AE004983.1	NT	Pseudomonas aeruginosa PA01, section 529 of the complete genome
10205	22700	35693	0.56	8.7E-01	BF570168.1	EST_HUMAN	80218554171 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309890 3'
10205	22700	35694	0.56	8.7E-01	BF570169.1	EST_HUMAN	80218554111 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309890 3'
10711	23239	36254	5.79	8.7E-01	BF3833970.1	EST_HUMAN	QV6-NN1021-106800-337-003 NN1021 Homo sapiens cDNA
11582	24028	37097	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4043584 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4043584 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
121468	24881			4.44	S.TE-01 AV681888.1	EST_HUMAN	AV681888 GLC Homo sapiens cDNA clone IMAGE/G073'
500	13132			1.55	S.8E-01 X17012.1	NT	Rat IgfII gene for insulin-like growth factor II
891	13505	28024		8.72	S.8E-01 W69089.1	EST_HUMAN	2d44e63.r1 Soares_fetal_heart_NbH-19W Homo sapiens cDNA clone IMAGE:343518 5'
2310	14882	27457		1.06	S.8E-01	4503210 NT	Homo sapiens cytochrome P450 subfamily XXVIA (steroid 27-hydroxylase, cerebroendothelial xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3681	16262	28750		0.78	S.8E-01 AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3870	18488	28931		1.38	S.8E-01 U49724.1	NT	Drosophila melanogaster merlin (Dmefin) mRNA, complete cds
8057	18874	31415		9.06	S.8E-01 X60547.1	NT	Chicken lipoprotein lipase gene
8057	18874	31416		9.06	S.8E-01 X60547.1	NT	Chicken lipoprotein lipase gene
8810	19401	32216		1.88	S.8E-01 AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
8810	19401	32217		1.88	S.8E-01 AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410			1.33	S.8E-01 AP001618.1	NT	Bacillus halodurans genomic DNA, section 1214.
7886	20528	33434		0.54	S.8E-01 AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9603	22103			0.48	S.8E-01 AE000878.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812			1.73	S.8E-01 AL112162.1	NT	Bordetella cihanes strain T4 cDNA library under conditions of nitrogen deprivation
6826	19416	32232		1.32	S.5E-01 AF185214.1	NT	Bacteriophage D3, complete genome
7533	20053	32828		2.38	S.5E-01 BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7832	20474	33383		0.51	S.5E-01 AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
6557	20897	33817		0.84	S.5E-01 P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818		0.84	S.5E-01 P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20881	33888		0.51	S.5E-01 AJ242213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10252	22747	35734		1.38	S.5E-01 AB006788.1	NT	Cyanidium caldarium gene for SgC, complete cds
10252	22747	35735		1.38	S.5E-01 AB006789.1	NT	Cyanidium caldarium gene for SgC, complete cds
120277	24978			3.12	S.5E-01 11418543	NT	Homo sapiens human immunodeficiency virus type 1 (HIVP1), mRNA
12084	24955			7.92	S.5E-01 9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
44882	17440	23890		0.62	S.4E-01 AF083975.2	NT	FoxI adenosin 8, complete genome
56885	24747	30807		3.15	S.4E-01 L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
56885	24747	30808		3.15	S.4E-01 L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
98888	22365			2.68	S.4E-01 AJ248287.1	NT	Pynococcus abyssi complete genome; segment 5/8
771	13390	25889		2.48	S.3E-01 M63437.1	NT	Thermus thermophilus cytochrome c-552 (cytB) and CydB (cytB) genes, complete cds
31228	15743	28212		3.28	S.3E-01 AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3683	16481	28943		0.66	S.3E-01 AB010379.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	16880	29140		3.24	S.3E-01 Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5473	18107	30428		2.15	S.3E-01 AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087			3.14	8.3E-01 AI791852.1	EST_HUMAN	mn01112.36 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1078465 5' similar to contains THR, H, THR repetitive element;
10019	22514	35507		1.11	8.3E-01 AF088070.1	NT	Drosophila melanogaster Ls1 homolog mRNA, complete cds
10119	22614	35604		3.5	8.3E-01 AF108153.1	NT	Mus musculus neurod4 gene, exons 3 through 12 and partial cds
10563	23089	36103		2.92	8.3E-01 AE000003.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 108 of 148) of the complete genome
10571	23108			2.52	8.3E-01 7212472	NT	Phytophthora infestans mitochondrial, complete genome
11183	29888	36735		2.45	8.3E-01 AF020503.1	NT	Homo sapiens FRA2B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2098	14875	27244		3.23	8.2E-01 AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715			1.45	8.2E-01 AF145589.1	NT	Mus musculus trophin (Ttn) gene, complete cds
3989	16567	29036		1.12	8.2E-01 AB014574.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
4209	16798	28246		0.81	8.2E-01 Z72584.1	NT	S cerevisiae chromosome VII reading frame ORF YGL022W
4209	16798	28247		0.81	8.2E-01 Z72584.1	NT	S cerevisiae chromosome VII reading frame ORF YGL022W
5270	17832	30258		1.08	8.2E-01 AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17977	30385		2.11	8.2E-01 AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	19805	32439		0.8	8.2E-01 AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
6978	19554	32379		3.18	8.2E-01 AW3709433.1	EST_HUMAN	CM4-HT10243-0811880-037-e01 HT0243 Homo sapiens cDNA S.cerevisiae MET, LEU4, and P01.1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7313	24778	32700		4.21	8.2E-01 Z12126.1	NT	
9838	22433	35409		0.63	8.2E-01 AB014530.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
9971	22468	35450		1.67	8.2E-01 AF052859.1	NT	Homo sapiens fibroblastin-related protein mRNA, complete cds
10123	22818	35689		0.59	8.2E-01 AF223888.1	NT	Oncorhynchus tshawytscha isolata T-20 somatotactin precursor gene, exon 1
10123	22818	35810		0.59	8.2E-01 AF223888.1	NT	Oncorhynchus tshawytscha isolata T-20 somatotactin precursor gene, exon 1
10286	22781	35772		3.52	8.2E-01 Q8JU70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773		3.52	8.2E-01 Q8JU70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11498	23847	37017		3.33	8.2E-01 L10127.1	NT	MDuscum contagiosum virus type 1 ORF1 and ORF2 DNA
41576	24022	37091		8.05	8.2E-01 P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24029	37089		5.68	8.2E-01 H87398.1	EST_HUMAN	yr14d02.11 Saccharomyces_cerevisiae_BioPowers_2NtBP8to9W Homo sapiens cDNA clone IMAGE:2521985 5' similar to g3:M26072 80S RIBOSOMAL PROTEIN L7A (HUMAN);
12102	24384	30970		1.86	8.2E-01 AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2787	16340			1.79	8.1E-01 AF181839.1	NT	Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds
3504	16109	28585		2.98	8.1E-01 AF065068.1	NT	Homo sapiens MHC class 1 region
3504	16109	28586		2.98	8.1E-01 AF065068.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
5046	17819		0.68	8.1E-01 AF202634.1	NT	Drosophila melanogaster Na/KATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds	
6457	18058	31843	0.88	8.1E-01 U16790.1	NT	Mus musculus putative collagen alpha-2 (X) chain (COL11A2) gene, partial cds	
6735	18328	32134	2.54	8.1E-01 Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M3-B	
6735	18328	32135	2.54	8.1E-01 Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M3-B	
7852	20394	33298	0.84	8.1E-01 AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Piout) gene, partial cds; putative sodium channel (NaCh) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds	
7852	20394	33299	0.84	8.1E-01 AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Piout) gene, partial cds; putative sodium channel (NaCh) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds	
8545	21084	34008	0.92	8.1E-01 AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14	
8545	21084	34007	0.92	8.1E-01 AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14	
8705	21244	34167	1.08	8.1E-01 AW242847.1	EST_HUMAN	nr01hc3.j1 NCI CGAP_Kdh1 Homo sapiens cDNA clone IMAGE:2892468 3' similar to SW1LYAR_MOUSE_Q08288 CELL GROWTH REGULATING NUCLEAR PROTEIN; contains MER22.61 PTR5 repetitive element	
10032	22627	35522	0.54	8.1E-01 P08425	SWISSPROT	PROBABLE E4 PROTEIN	
11356	23810	36869	2.97	8.1E-01 BE838558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	
11356	23810	36870	2.97	8.1E-01 BE838558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	
11811	24183	31031	3.32	8.1E-01 AE001711.1	NT	Thermotoga maritime section 23 of 38 of the complete genome	
188	12849		4.98	8.0E-01 AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acyltransferase allele 16	
310	12965	25453	7.95	8.0E-01 AJ132772.1	NT	Bos taurus fibub and rfb genes	
2080	14681		1.47	8.0E-01 BF530982.1	EST_HUMAN	602072473F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215081 5'	
3113	15728	28189	1.24	8.0E-01 AF1227987.1	NT	Salinaria bohemicana olfactory receptor (SBO27) gene, partial cds	
3354	15882	28439	1.13	8.0E-01 AB008183.1	NT	Mus musculus gene for oxiductal glycoprotein, complete cds	
3766	16386		1.05	8.0E-01 AL162758.2	NT	Netsseria meningitis serogroup A strain Z261 complete genome; segment 7/7	
4630	17213	28964	5.65	8.0E-01 X83759.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	
5117	17689	30127	1.09	8.0E-01 7657352	NT	Mus musculus myosin IBb (Myo5b), mRNA	
7831	20473		2.32	8.0E-01 AW801488.1	EST_HUMAN	RC0-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA	
8462	21002	33919	1.17	8.0E-01 Y1085.1	NT	Rice stripe virus RNA 3	
479	13112	25602	1.37	7.9E-01 D11473.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	
744	13384		1.05	7.9E-01 AE002130.1	NT	Unoplasmodia ureolyticum section 31 of 59 of the complete genome	
1848	14240		28.9	7.9E-01 AB040865.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds	
1895	14288		1.11	7.9E-01 U322739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome	
2303	14878	27452	6.78	7.9E-01 AB004816.1	NT	Oncorhynchus kisutchus mRNA for mitsugumin29, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.9E-01 AF130459.1	NT	Danio rerio Tsp4-associated protein Tap1A (tap1A) mRNA, complete cds	
3587	16171	28653	2.33	7.9E-01 AF228884.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	
4389	16875		0.76	7.9E-01 BE283612.1	EST_HUMAN	6011620235F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'	
4717	17298	28743	1.04	7.9E-01 6753745	NT	Mus musculus embbin (Emb) mRNA	
4717	17298	28744	1.04	7.9E-01 6753745	NT	Mus musculus embbin (Emb) mRNA	
5315	17877		5.8	7.9E-01 M28830.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17	
6485	19088	31888	0.89	7.9E-01 D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds	
8053	20595	33502	2.62	7.9E-01 X96898.1	NT	P.satiuum GR gene	
9466	21891	34948	4.57	7.9E-01 U01812.1	NT	Giardia lamblia variant-4-specific surface protein G3M4-B (gapG3M4-B) mRNA, partial cds	
8962	22457	35440	4.27	7.9E-01 P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN	
10003	22498	35487	0.75	7.9E-01 AV700880.1	EST_HUMAN	AV700880 GKC Homo sapiens cDNA clone GKCDRE123'	
10405	22898	35894	0.71	7.9E-01 AB000831.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thiomannose reductase, complete cds	
10886	23407		2.28	7.9E-01 7682471	NT	Human sapiens KIAA1072 protein (KIAA1072) mRNA	
11089	23801	36839	2.72	7.9E-01 P18022	SWISSPROT	NEURAL-CAUDHERIN PRECURSOR (N-CADHERIN)	
909	13222		1.4	7.9E-01 Z43785.1	EST_HUMAN	HSCHKH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04	
2314	14888	27481	14	7.9E-01 AW888867.1	EST_HUMAN	EST371687 MAGE gene sequences, MAGF Homo sapiens cDNA	
4811	17389	28840	0.81	7.9E-01 U87205.1	NT	Rattus norvegicus transmembrane receptor Unsh1 mRNA, complete cds	
5189	17754		0.81	7.9E-01 AW753353.1	EST_HUMAN	RC3-CT1254-130100-022 C1254 Homo sapiens cDNA	
6219	18820	31603	2.33	7.9E-01 AF115896.1	NT	Sphingonotus alpha endopeptidase mRNA, partial cds	
6387	18871	31750	1.05	7.9E-01 P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)	
6589	19188	31888	0.75	7.9E-01 AL445068.1	NT	Thermoplasma acidophilum complete genome; segment 4/5	
8428	20988	33881	1.04	7.9E-01 BF108927.1	EST_HUMAN	7154d05.31 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'	
9160	21895	34839	1.02	7.9E-01 Y10159.1	NT	Drosophila melanogaster gap gene	
8255	21781	34733	0.53	7.9E-01 4826873	NT	Homo sapiens nucleophosmin 214D (CAIN) (NUP214) mRNA	
10031	22528		0.78	7.9E-01 Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (VDL-ALPHA1)	
12071	24857		2.33	7.9E-01 L28260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopentanecarboxylate synthase (ACS5) gene, complete cds	
150	12213	25300	4.65	7.7E-01 AF184345.1	NT	Lycopodium Hirsutum ADP-glucose pyrophosphorylase large subunit (AGPL1) mRNA, complete cds	
755	13374		1.44	7.7E-01 AF050157.1	NT	Mus musculus major histocompatibility protein class II alpha chain (IAlpha) and major histocompatibility protein class II beta chain (IEBeta) genes, complete cds; butyrophilin-like (NC8); butyrophilin-1p	
2737	15282	27880	2.33	7.7E-01 O33915	SWISSPROT	CITRATE SYNTHASE	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.62	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosaminepolypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4489	17071	28521	3.17	7.7E-01	AF168488.1	NT	Catarrh catarrh japonica sub-species japonica beta-actin mRNA, partial cds
4488	17071	28522	3.17	7.7E-01	AF168488.1	NT	Catarrh catarrh japonica sub-species japonica beta-actin mRNA, partial cds
6749	18376	31084	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18728	31479	0.8	7.7E-01	R08600.1	EST_HUMAN	yf24002_s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:12775_3'
8758	22258	36239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
4780	17370	28822	19.73	7.6E-01	L27316.1	NT	Oryctodileus curicus immunoglobulin VDJ region gene
4780	17370	28823	19.73	7.6E-01	L27316.1	NT	Oryctodileus curicus immunoglobulin VDJ region gene
6248	18857	31628	4.81	7.6E-01	AF056510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylese non-biotinylated subunit (MCCB) mRNA, complete cds
6248	18857	31629	4.81	7.6E-01	AF056510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylese non-biotinylated subunit (MCCB) mRNA, complete cds
6841	19237	32039	0.7	7.6E-01	P37688	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA 2A
6935	18043	30485	0.95	7.6E-01	AI253389.1	EST_HUMAN	sq14b12.2 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2630879
6935	18043	30488	0.95	7.6E-01	AI253389.1	EST_HUMAN	sq14b12.2 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2630879
7113	19453	32269	0.98	7.6E-01	U72487.1	NT	Rattus norvegicus cadmium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.6E-01	AF146793.2	NT	Mus musculus neuregulin U precursor (NmU) gene, partial cds; PPNL_P (Tpnp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pf27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8068	20610	33522	1.78	7.6E-01	6857752	NT	Mus musculus adhillin (Adhl-pending), mRNA
8068	20610	33523	1.78	7.6E-01	6857752	NT	Mus musculus adhillin (Adhl-pending), mRNA
8237	20808	33727	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NMDAR2C)
8237	20808					SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NMDAR2C)
8897	21435	34359	0.81	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2B9, phorbol ester inducible, type a (Cyp2b9), mRNA
9203	21720	34684	3.33	7.6E-01	P303172	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34685	3.33	7.6E-01	P303172	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23176	36824	2.74	7.6E-01	X86347.1	NT	H.aspera mRNA for neurofilament NF70
11236	23176	36825	2.74	7.6E-01	X86347.1	NT	H.aspera mRNA for neurofilament NF70

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11556	24004			6.74	7.6E-01 AL161682.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 88
11711	24121			6.31	7.6E-01 AB020702.1	NT	Homo sapiens mRNA for KIAA0885 protein, partial cds
539	13170			1.32	7.5E-01 AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.5E-01 AF020503.1	NT		Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7530	20050	32823	0.74	7.5E-01 AF052730.1	NT		Drosophila melanogaster tyrosine kinase receptor protein (opt) mRNA, complete cds
12027	24318			5.20	7.5E-01 AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30897	1.91	7.5E-01 D80807.1	NT		Synaptotagmin sp. PCG8503 complete genome, 8/27/1058467-1/188885
1169	13771	262779	1.38	7.4E-01 AL588148.1	EST_HUMAN		ln14b09_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains AU repetitive element;contains element MIR repetitive element:
3789	16389	28854	0.83	7.4E-01 AF112638.1	NT		Machaerina pusilla actin (Act1) mRNA, complete cds
4400	16835	29430	7.7	7.4E-01 AL163248.2	NT		Homo sapiens chromosome 21 segment HS21C048
7785	20328	33234	1.03	7.4E-01 AL161551.2	NT		Arabidopsis thaliana DNA chromosome 4, coding fragment No. 51
7785	20328	33235	1.03	7.4E-01 AL161551.2	NT		Arabidopsis thaliana DNA chromosome 4, coding fragment No. 51
8568	21107	34028	0.83	7.4E-01 BF346268.1	EST_HUMAN		602018456871 NCI CGAP_Bm87/Homo sapiens cDNA clone IMAGE:4154340 5'
8847	21180		0.64	7.4E-01 US7880.1	NT		Pettus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9028	21563	34492	7.17	7.4E-01 BE747503.1	EST_HUMAN		60157302651 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:38341174 5'
8083	21619	34554	1.19	7.4E-01 AA187886.1	EST_HUMAN		Zp67101.81 Strategene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:655297 3' similar to SW:TCPQ_MOUSE_P42882 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10301	22795	35798	0.59	7.4E-01 11424633	NT		Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11516	23964	37034	1.68	7.4E-01 AB021480.2	NT		Oryzias latipes gene for membrane guanylyl cyclase OGGC1, complete cds
11516	23964	37035	1.68	7.4E-01 AB021480.2	NT		Oryzias latipes gene for membrane guanylyl cyclase OGGC1, complete cds
11677	24098		4.11	7.4E-01 6753217	NT		Mus musculus complement component 1 inhibitor (C1inh), mRNA
11784	241176		1.28	7.4E-01 AJ472841.1	EST_HUMAN		tar3h01_x1 NCI CGAP_Lymf5 Homo sapiens cDNA clone IMAGE:2043885 3'
4723	17304	28748	0.72	7.3E-01 AE001168.1	NT		Bacillus burgdorferi (section 52 of 70) of the complete genome
4810	17388	28839	2.83	7.3E-01 AF225421.1	NT		Homo sapiens HT017 mRNA, complete cds
6260	17823	30248	0.89	7.3E-01 O43103	SWISSPROT		FERRICHROME SIDEROPORE PEPTIDE SYNTHETASE
6720	18314	32116	5.88	7.3E-01 L35772.1	NT		Mus musculus antigen (CD72) gene
6720	18314	32117	5.88	7.3E-01 L35772.1	NT		Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01 AJ011418.1	NT		Lycopersicon esculentum mRNA for ubiquitin activating enzyme
7549	20068	32942	7.77	7.3E-01 M28511.1	NT		Valignolobius sucrose (scrB) gene, complete cds
7549	20068	32943	7.77	7.3E-01 M28511.1	NT		Valignolobius sucrose (scrB) gene, complete cds
11307	23800	36859	3.88	7.3E-01 AA678019.1	EST_HUMAN		Zic2b03_s1 Scores_fetal_liver_scores cDNA clone IMAGE:431789 3'

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11307	23800	36880	3.88	7.3E-01	AA878018.1	EST HUMAN	z255008_s1 Soares_fetal_liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:4317983'
884	13479		1.68	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X78140.1	NT	N.tabacum Nelf-4A13 mRNA
2501	15085	27639	1.38	7.2E-01	AB009805.1	NT	Geitius galiius gene for melanocortin 2-receptor, complete cds
3103	15718	281188	1.28	7.2E-01	AF108100.1	NT	Foxipox virus, complete genome
3500	16105	28590	2.97	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (esp417-8) gene, esp417-8/A-I allele, complete cds
3940	16538	28005	1.81	7.2E-01	BF328350.1	EST_HUMAN	602035589F1 NCI_CGAP_Bm64_Homo sapiens cDNA clone IMAGE:4183222_5'
4185	16775	28222	0.6	7.2E-01	U02568.1	NT	Dicynocaritus wiparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
4884	17459	28911	2.54	7.2E-01	D80314.1	NT	L.mesenteroides gene for sucrose phosphorylase [EC 2.4.1.7]
5348	17908	303123	0.9	7.2E-01	AF158690.2	NT	Streptococcus thermophilus bacteriophage Sfi11, complete genome
5388	17945	30358	0.69	7.2E-01	AL161583.2	NT	Anabiosis thalana DNA chromosome 4, contig fragment No. 63
7265	19753	32649	0.82	7.2E-01	U89833.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8391	20921	33851	1.15	7.2E-01	AF238081.1	NT	Oryctodius curicus RING-finger binding protein mRNA, partial cds
8883	21451		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06_5'
10243	22738	35729	2.14	7.2E-01	BF670081.1	EST_HUMAN	60211838F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4275391_5'
10618	23150	36162	5.23	7.2E-01	UR28232.1	NT	Rateus norvegicus cytochrome c mRNA, complete cds
12037	16775	29222	1.88	7.2E-01	U02568.1	NT	Dicynocaritus wiparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12233	24449		4.42	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
12268	24969		1.67	7.2E-01	Y10168.1	NT	B.thuringiensis PK1 & cap genes, putative
721	13341	25831	10.58	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullofring skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3098	15713	28185	18.71	7.1E-01	A1270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 1-5-16
4287	16813	28921	4.11	7.1E-01	7305360	NT	Mus musculus cogenin (Otag), mRNA
4287	16813	28922	4.11	7.1E-01	7305360	NT	Mus musculus cogenin (Otag), mRNA
6103	18719	31471	1.81	7.1E-01	BF881034.1	EST_HUMAN	6021185438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344_5'
6103	18719	31472	1.81	7.1E-01	BF881034.1	EST_HUMAN	6021185438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344_5'
7029	18583	32380	6.04	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropharn synthase (pr) gene, complete cds
8132	20673	33584	0.53	7.1E-01	HS4244.1	EST_HUMAN	3888409_s1 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:2029813'
8871	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-d09 BT0567 Homo sapiens cDNA
8871	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-d09 BT0567 Homo sapiens cDNA
9768	22287	35252	1.48	7.1E-01	BE004405.1	EST_HUMAN	601498330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495_5'
10309	22803	35705	1.08	7.1E-01	M12081.1	NT	Human T-cell receptor germline germline-chain J2 gene
12012	24878		2.58	7.1E-01	AA421482.1	EST_HUMAN	zu06111_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109_3'

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Probe SEQ ID NO:	Exn SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	138688	28387	1.3	7.0E-01 AB014514.1	NT		Homo sapiens mRNA for KIAA0814 protein, partial cds	
1272	138688	28389	1.3	7.0E-01 AB014514.1	NT		Homo sapiens mRNA for KIAA0814 protein, partial cds	
2492	15057	27030	1.22	7.0E-01 NC2412.1	EST_HUMAN		yZ73e07.s1 Scores_multiple_scenarios_2NBH-HMSP Homo sapiens cDNA clone IMAGE:2887078 3' similar to contains Alu repetitive element	
2492	15057	27631	1.22	7.0E-01 N62412.1	EST_HUMAN		yZ73e07.s1 Scores_multiple_scenarios_2NBH-HMSP Homo sapiens cDNA clone IMAGE:2887078 3' similar to contains Alu repetitive element	
5213	17778		1.98	7.0E-01 AL163301.2	NT		Homo sapiens chromosome 21 segment HS2TC101	
5382	17922	30338	2.89	7.0E-01 AE003892.1	NT		Xylella fastidiosa, section 87 of the complete genome	
6107	18723		1.03	7.0E-01 AB021316.1	NT		Arabidopsis thaliana mRNA for chitinophil b synthase, complete cds	
8319	20890		11.92	7.0E-01 AE000253.1	NT		Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome	
8240	21768	34714	0.61	7.0E-01 U53988.1	NT		Clostridium acetobutylicum manitut-specific phosphotransferase system (PTS) system, mtaA, mtaR, mtf, and mtD genes, complete cds	
8240	21768	34715	0.61	7.0E-01 U53988.1	NT		Clostridium acetobutylicum manitut-specific phosphotransferase system (PTS) system, mtaA, mtaR, mtf, and mtD genes, complete cds	
108990	22513	38548	1.99	7.0E-01 AV763842.1	EST_HUMAN		AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'	
108990	22513	38547	1.89	7.0E-01 AV763842.1	EST_HUMAN		AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'	
12594	24818	30715	1.35	7.0E-01 8630464	NT		Bacteriophage N15 virion, complete genome	
1005	13816	28130	10.2	6.9E-01 U68674.1	NT		Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds	
1005	13816	28131	10.2	6.9E-01 U68674.1	NT		Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds	
1353	13848	28472	2.8	6.9E-01 AA562530.1	EST_HUMAN		mn28a628.81 NCI CGAP Gen1 Homo sapiens cDNA clone IMAGE:1083176 3'	
3256	158688	28348	1.7	6.9E-01 AE002271.2	NT		Chlamydia muridarum, section 3 of 85 of the complete genome	
5854	18276	31310	0.8	6.9E-01 AB035862.1	NT		Branchiosoma belcheri BBNAA3 mRNA for neobehard actin, complete cds	
6508	19108	31893	1.31	6.9E-01 BE288188.1	EST_HUMAN		60117733SF1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'	
7821	20483	33369	3.4	6.9E-01 AL161573.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	
7821	20483	33370	3.4	6.9E-01 AL161573.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	
9098	21634		0.83	6.9E-01 AF118046.1	NT		Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds	
9811	22111	35073	0.62	6.9E-01 AF208319.1	NT		Musa acuminata peptidase lyase 1 (PL1) mRNA, complete cds	
9811	22111	35074	0.62	6.9E-01 AF208319.1	NT		Musa acuminata peptidase lyase 1 (PL1) mRNA, complete cds	
10307	22801	35793	0.86	6.9E-01 BF242367.1	EST_HUMAN		601860580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108419 5'	
11138	23648	36887	1.94	6.9E-01 D89013.1	NT		Homo sapiens DAN gene, complete cds	
11138	23648	36888	1.94	6.9E-01 D89013.1	NT		Homo sapiens DAN gene, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11851	24870			2.3E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1)(MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
12670	25003	308111		6.9E-01	AI888312.1	EST_HUMAN	wn31f02.x1 NCI CGAP_Cat4 Homo sapiens cDNA clone IMAGE:2447087 3'
982	13604	28118		6.8E-01	AF017784.1	NT	Giardia intestinalis carboxyl kinase gene, complete cds
2698	15265			1.2E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/21, 3418852-3573470
2858	14249	26783		6.8E-01	AA854475.1	EST_HUMAN	q75a05.s1 Scores_parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1402258 3' similar to gb:X58411_ma1 AlCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN); gb:X58411_ma1
4872	17254	29708		6.8E-01	J007622.1	NT	Rat(hooded) plectin gene : exon iii and flanks
8558	22098	35017		6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10281	22798			0.4E-01	AA687038.1	EST_HUMAN	mv13e07.s1 NCI CGAP_Pi22 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13548_ma1
10985	23480	36505		6.8E-01	AJ278675.1	NT	Human HMG-17 gene for non-Histone chromosomal protein (HUMAN); Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-
10985	23480	36506		2.9E-01	AJ278675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-
10983	23507	36540		6.8E-01	AF038339.1	NT	Mus musculus zinc finger protein (P-eg3) mRNA, complete cds
10983	23507	36541		2.1E-01	AF038339.1	NT	Mus musculus zinc finger protein (P-eg3) mRNA, complete cds
11178	23884	36730		6.8E-01	AF164161.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11475	23925	36895		1.7E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RacGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11475	23925	36896		6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RacGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
320	12074	25483		27.63	6.7E-01	AF213884.1	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
361	13010	25485		1.77	6.8E-01	AF110520.1	NT
1985	14539			0.97	6.7E-01	M12132.1	Quail fast skeletal muscle troponin I gene, complete cds
2192	14768	27340		1.65	6.7E-01	AA451884.1	EST_HUMAN
2211	15460	27351		2.68	6.7E-01	AF188073.1	Drosophila melanogaster Msat5SC gene, complete cds; NM0045 Isoform (Nmndmc) gene, complete cds, alternatively spliced; and transcription factor (Retinoid) gene, complete cds, alternatively spliced
3028	15642	28120		4.28	6.7E-01	6878580	NT
4550	17133	28581		0.84	6.7E-01	X74421.1	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
							S.tuberosum mRNA for glucose-6-phosphate dehydrogenase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Descriptor
5100	17672	30111	0.98	6.7E-01	AW079110.1	EST_HUMAN	des25g12.x1 NCI_CGAP_Cof17 Homo sapiens cDNA clone IMAGE:2574598 3'	
5700	18328	30828	0.8	6.7E-01	J04838.1	NT	M. berkeni ATPase alpha and beta subunit (atpA and atpB) genes, complete cds	
5700	18328	30830	0.8	6.7E-01	J04838.1	NT	M. berkeni ATPase alpha and beta subunit (atpA and atpB) genes, complete cds	
6118	18732	31495	0.83	6.7E-01	AED001486.1	NT	Helicobacter pylori, strain J89 section 47 of 132 of the complete genome	
6465	18068	31851	1.65	6.7E-01	9835035	NT	Gallid herpesvirus 2, complete genome	
6465	18068	31852	1.55	6.7E-01	9835035	NT	Gallid herpesvirus 2, complete genome	
7358	18882		4.12	6.7E-01	AED04606.1	NT	Pseudomonas aeruginosa PA01, section 187 of 529 of the complete genome	
7378	18904	32798	0.9	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J89 section 47 of 132 of the complete genome	
10049	22544		0.87	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds	
10832	23353	38398	2.52	6.7E-01	BFS554649.1	EST_HUMAN	CMS-HT0789-0106900-197->3 HT0789 Homo sapiens cDNA	
11333	23031	36040	3.45	6.7E-01	O14237	SWISSPROT	N-ACETYL GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11	
2546	15110	27682	2.68	6.5E-01	AF075240.1	NT	Homo sapiens SLC1 protein (SLC12) mRNA, partial cds	
2724	15270	27846	1.01	6.5E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds	
3559	16141	28623	1.35	6.5E-01	4508889	NT	Homo sapiens same domain, seven transmembrane repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	
3719	16320	28788	3.42	6.5E-01	Y07888.1	NT	Cathecas random DNA marker, 222bp	
4187	16777		0.87	6.5E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoR γ T gene, and sodium phosphate transporter (NPT3) gene, complete cds	
5227	17781	30210	0.97	6.5E-01	AI218230.1	EST_HUMAN	ch23a10x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845488 3' similar to contains PTR5.12 MER28 repetitive element:	
6474	18075	31858	4.22	6.5E-01	68890577	NT	Mus musculus kinase light chain 2 (Klc2), mRNA	
7875	20188	33074	3.61	6.5E-01	AV860508	EST_HUMAN	AV860508 GlcNAc cDNA clone GLCGID04 3'	
8501	21040	33981	0.64	6.5E-01	AV704700	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ABCA11 5'	
8582	22082		1.73	6.5E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
8915	22411		0.68	6.5E-01	AU1118198.1	EST_HUMAN	AU1118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'	
12118	24377	30973	1.27	6.5E-01	AF110001.1	NT	Homo sapiens glutamate cyclase activating protein 3 (GCAP2) gene, exon 4 and complete cds	
651	13274	23751	1.12	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds	
651	13274	23752	1.12	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds	
3480	16088	28560	5.04	6.5E-01	AB041225.1	NT	Mus musculus gene for Tab2, complete cds	
4110	16704	28157	1.1	6.5E-01	4504632	NT	Homo sapiens Interleukin 10 receptor, alpha (IL10RA) mRNA	
4289	16656	28398	3.29	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	
4699	17281	28728	1.28	6.5E-01	D00584.1	NT	Oryza sativa gene for propro-glutelin, exons 1, 2, 3, 4, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	302022	2.39	6.5E-01	U28921.1	NT	<i>Phascolinus vulgaris</i> ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5336	17887	30312	1.02	6.5E-01	Z70628.1	NT	<i>H. sapiens</i> mRNA for Immunoglobulin heavy chain variable region (9DA-A8, VH4, 4-59)DP-71)
6825	18415	32231	1.28	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosome matrix protein, complete cds
7883	20175	33062	0.88	6.5E-01	A1786882.1	EST_HUMAN	wc46a02x1 NCI CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2321642 3'
9751	22249		1.25	6.5E-01	T78904.1	EST_HUMAN	y21b04.11 Scores fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35725	2.48	6.5E-01	AF119876.1	NT	<i>Mus musculus</i> small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36061	3.35	6.5E-01	H87582.1	EST_HUMAN	yw17008.11 Scores placenta, StoerkeWeeks_2NbHTP8te9W Homo sapiens cDNA clone IMAGE:252515 5'
10568	23102	36118	4.35	6.5E-01	AA6001287.1	EST_HUMAN	ncf5c07.81 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10669	23201		4.20	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11470	23820	36889	2.7	6.5E-01	AF014115.1	NT	Plasmidium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes, encoding mitochondrial proteins, complete cds
12067	24348		8.24	6.5E-01	BE485050.1	EST_HUMAN	hv74e10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12221	24817		3.04	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL087C
273	12890	25417	9.34	6.4E-01	U48848.1	NT	<i>Drosophila melanogaster</i>
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	<i>Mus musculus</i> dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16528	28683	1.33	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA16017 protein, partial cds
4591	17174	28619	0.88	6.4E-01	Y12488.1	NT	<i>M. musculus</i> whn gene
4591	17174	28620	0.88	6.4E-01	Y12488.1	NT	<i>M. musculus</i> whn gene
6402	17880	30311	0.97	6.4E-01	AE002551.2	NT	<i>Neisseria meningitidis</i> serogroup B strain MC58 section 163 of 206 of the complete genome
8549	21088	34010	1.78	6.4E-01	AE001247.1	NT	Tropaeolum pelatum section 83 of 87 of the complete genome
10001	22498	35486	8.23	6.4E-01	U82828.1	NT	<i>Homo sapiens</i> atelocollagenase (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF670405.1	EST_HUMAN	6021501288FT NIH_MGC_81 Homo sapiens cDNA clone MDSCG320B 5'
12188	24420		29.97	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCG320B 5'
459	13083	25537	3.73	6.3E-01	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
569	13101	25880	59.3	6.3E-01	U32689.1	NT	<i>Haemophilus influenzae</i> Rd section 4 of 163 of the complete genome
2207	14783	27356	3.24	6.2E-01	U81138.1	NT	<i>Shigella flexneri</i> multi-antibiotic resistance locus
2814	15178	27744	2.78	6.3E-01	U75331.1	NT	<i>Gallus gallus</i> bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2814	15178	27745	2.78	6.3E-01	U75331.1	NT	<i>Gallus gallus</i> bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15663		0.75	6.3E-01	Y17275.1	NT	Lycopetinol esculentum p58a gene, complete CDS
6214	18824	31525	0.78	6.3E-01	BE083806.1	EST_HUMAN	PMD-BT0757-010500-002-405 BT0757-Homo sapiens cDNA
6712	18208	32110	1	6.3E-01	L27788.1	NT	Streptococcus dysgalactiae (mog) gene, complete cds
6712	18208	32111	1	6.3E-01	L27788.1	NT	Streptococcus dysgalactiae (mog) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20908			3.32	6.3E-01 BE002044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858351 5'
8819	21358	34284	0.91	6.3E-01 S62827.1	NT		glycoprotein IIIa [Alu 1 and 3 fusion junction] [Human, Genomic: Murein, 300 nt]
9147	21682	34627	1.15	6.3E-01 BF216894.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'	
9341	21855	34804	2.9	6.3E-01	9827521	NT	Venda virus, complete genome
9341	21855	34805	2.0	6.3E-01	9827521	NT	Venda virus, complete genome
9851	22349		0.67	6.3E-01 AE002329.2	NT		Chlamydia muridarum, section 69 of 85 of the complete genome
10324	22818	35814	1.52	6.3E-01 Z79883.1	NT		S.cerevisiae chromosome VII reading frame ORF YGR216w
10421	22816	35916	0.87	6.3E-01 AE000213.1	NT		Euchromatin cell K-12 MG1655 section 203 of 400 of the complete genome
10839	23458	38478	2.45	6.3E-01 AA877715.1	EST_HUMAN	CM-BT043-080289-046 BT043 Homo sapiens cDNA	
11216	23719	38773	15.21	6.3E-01 AI904160.1	EST_HUMAN	CM-BT043-080289-046 BT043 Homo sapiens cDNA	
11302	23795	36885	1.94	6.3E-01 IP47033	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION	
11458	23808	36973	2.02	6.3E-01 P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION	
11769	25042	30505	30.63	6.3E-01	8810283	NT	Mus musculus keratin complex 2, gene 8g (Krt2-8g), mRNA
11884	24219		1.85	6.3E-01 AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfatase synthetase (PAPS) mRNA, complete cds	
12082	24953		3.2	6.3E-01 X83528.1	NT	Clinical paed gene	
5175	17742	30171	0.71	6.2E-01 AF167898.1	NT	Spermophilus suslicus lsidato S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for	
6030	18649	31390	2.03	6.2E-01 Q10135	SWISSPROT	mitochondrial product	
7506	20228		3.14	6.2E-01 AF022253.1	NT	HYPOTHETICAL C23E2.02 IN CHROMOSOME 1	
7548	24788	32941	1.08	6.2E-01 AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds	
8243	20784	33703	5.65	6.2E-01 H72255.1	EST_HUMAN	Swine fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542.3'	
8780	21329	34254	0.54	6.2E-01 AF034411.1	NT	Mus musculus chromosomal X contigA; putative Magess gene, Caltracin, NAD(P) steroid dehydrogenase and Zinc finger protein 185	
88370	20308	33212	1.75	6.2E-01 BE562687.1	EST_HUMAN	Lyopersicon esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds	
89429	21938		2.35	6.2E-01 M244491.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds	
89890	22485	35472	6.85	6.2E-01 AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23	
10428	22823	35927	3.76	6.2E-01 P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]	
10428	22823	35928	4.95	6.1E-01	6678076	NT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2438	15005		1.05	6.1E-01	4557538	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
46832	17215	28688	1.05	6.1E-01		Human sepius sulfate carrier family 28 (sulfate transporter), member 2 (SLC28A2) mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Database Source	Top Hit Descriptor
6141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypyridinylbenzoate methyltransferase mRNA, complete cds	
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypyridinylbenzoate methyltransferase mRNA, complete cds	
5727	18353	31057	1.54	6.1E-01	M58840.1	NT	Ceanothobabtis elegans N2 CefMyD (hrh-1) alternatively spliced genes, complete cds	
6951	19528	32351	3.55	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds	
6951	19528	32352	3.56	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds	
8175	20716	33632	3.57	6.1E-01	AF055353.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds	
8739	21269	34187	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAPK4), mRNA	
8739	21269	34189	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAPK4), mRNA	
9338	21850	34789	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	
9338	21850	34790	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	
9758	22254	35226	1.15	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome	
8958	22454	35436	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	
10837	23358		8.53	6.1E-01	X74507.1	NT	P. sagittum mch mRNA for chloroplast malate dehydrogenase (NADP+)	
11581	24027	37085	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	
11581	24027	37098	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	
12530	24643		1.91	6.1E-01	X96287.1	NT	M.mazoi orfA, orfB, and orfC of archaeal ABC-transporter system	
520	13152	25835	1.46	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds	
587	13217		3.41	6.0E-01	5802889	NT	Homo sapiens adhesion-related protein complex 3, mu 2 subunit (CLA20), mRNA	
1406	13699	26528	1.93	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CHB9-53b attachment protein (G) gene, complete cds	
3887	18485	26946	0.86	6.0E-01	AJ233396.1	NT	Viral hemophagic sapovirus N, P, M, G, Nr, L genes, French strain 07-71	
4287	18553		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 28, 27, and 28	
5485	18119	30528	1.83	6.0E-01	F20298	SWISSPROT	D ₂ DOPAMINE RECEPTOR EST HUMAN	D ₂ DOPAMINE RECEPTOR EST HUMAN
5631	18290	30732	2.28	6.0E-01	AW139713.1	EST HUMAN	U1-H-B1-erb-a-10-Q-U1.31 NCI_OGAP_Sub3_Homo sapiens cDNA clone IMAGE:2718819.3'	U1-H-B1-erb-a-10-Q-U1.31 NCI_OGAP_Sub3_Homo sapiens cDNA clone IMAGE:2718819.3'
6980	19258	32059	3.73	6.0E-01	U28813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds	
6767	19360	32189	0.79	6.0E-01	Q04912	SWISSPROT	(CDW138) (CD138 ANTIGEN)	(CDW138) (CD138 ANTIGEN)
7391	19316	32780	5.28	6.0E-01	AJ277981.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	
8096	20088	33520	4.72	6.0E-01	PO2835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARazu	SEGMENTATION PROTEIN FUSHI TARazu
8096	20088	33521	4.72	6.0E-01	PO2835	SWISSPROT		
9737	22225	25214	2.22	6.0E-01	AB008183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22669			1.61	6.0E-01 Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
109346	23453	38478	2.14	6.0E-01 AJ31892.1	NT	Genus galus mRNA for Hyperon protein, 419 kD isoform	
109346	23453	38477	2.14	6.0E-01 AJ31892.1	NT	Genus galus mRNA for Hyperon protein, 419 kD isoform	
11428	23977	38942	2.84	6.0E-01 AA420223.1	EST_HUMAN	nt0807_x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:20956221 3'	
12158	24398	30978	1.82	6.0E-01 11421683 NT	Homosapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA		
12285	24475		1.69	6.0E-01 AA708087.1	EST_HUMAN	2188505.1 Soares fetal liver spleen 1NFLS ST1 Homo sapiens cDNA clone IMAGE:34827778 3'	
12428	24879		1.29	6.0E-01 5803138 NT	Homosapiens RNA binding motif protein 3 (RBM3), mRNA		
12469	24885	30709	2.49	6.0E-01 9055303 NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA		
12489	24810		6.92	6.0E-01 BE157817.1	EST_HUMAN	RC1-HT0375-030500-015-003 HT0375 Homo sapiens cDNA	
10338	13648	28160	1.09	5.9E-01 U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome	
1447	14039	28568	1.08	5.9E-01 68890232 NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgal), mRNA		
3308	15919	28395	5.12	5.9E-01 AL163267.2	NT	Homosapiens chromosome 21 segment HS21C087	
3308	15919	28398	5.12	5.9E-01 AL163267.2	NT	Homosapiens chromosome 21 segment HS21C087	
4304	168890		4.32	5.9E-01 AF162758.1	NT	Rattus norvegicus cendrin 2 mRNA, partial cds	
6591	19188	31981	1.48	5.9E-01 AF068440.2	NT	Homosapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds	
7310	18838	32698	5.58	5.9E-01 AB023486.1	NT	Homosapiens gene for histamine H2 receptor, promoter region and complete cds	
7841	20483	33395	0.57	5.9E-01 D80811.1	NT	Synchocystis sp. PCC6803 complete genome, 13/27_157563-1719843	
8462	21987	34943	0.93	5.9E-01 AF063204.2	NT	Chlamydia trachomatis strain KuW3/Co major outer membrane protein (omp1) gene, complete cds	
8827	22225		0.68	5.9E-01 P08483	SWISSPROT	E8 PROTEIN	
10081	22386	35578	1.15	5.9E-01 P66224	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)	
10351	23087	30102	3.24	5.9E-01 Q8X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)	
10557	23083	36105	1.75	5.9E-01 AF197844.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds	
10840	23381	36378	3	5.9E-01 AW827176.1	EST_HUMAN	PM1-DT0041-790100-002-H-N3 DT0041 Homo sapiens cDNA	
111073	23385	38828	2.25	5.9E-01 AF084628.1	NT	Mus sprattus strain SPRET/F1 CD48 antigen (Cd48) gene, partial cds	
111810	24182	31030	1.92	5.9E-01 AF42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region	
12053	24398		2.88	5.9E-01 AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds	
12280	24483		7.56	5.9E-01 P34928	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]	
1852	14538	27092	1.8	5.8E-01 P40472	SWISSPROT	SIM1 PROTEIN	
4058	168653	28119	1.22	5.8E-01 BF665738.1	EST_HUMAN	601852474F1 NIH_MCG_56 Homo sapiens cDNA clone IMAGE:40761315	
4612	17195	28841	3.73	5.8E-01 AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds	
4814	17498		1.18	5.8E-01 AF110846.1	NT	Megacephala scalaris sex-lethal homolog (Megax) gene, partial cds, alternatively spliced products	
5577	18208		0.75	5.8E-01 AE002152.1	NT	Ureaplasma urealyticum section S3 of 59 of the complete genome	

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
57722	18348	31051	2.52	5.8E-01	Q10689	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
63331	18937	31713	2.37	5.8E-01	D78859.1	EST_HUMAN	HUM500E068 Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E068 5'
64544	19055	31840	0.71	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
69003	19637		2.47	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
78228	20370		2.57	5.8E-01	I41571.1	EST_HUMAN	Ynr1b03.51 Soares adult brain N28SHB5Y Homo sapiens cDNA clone IMAGE-175757 3 similar to g: S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
80331	20573	33477	0.66	5.8E-01	A1280051.1	EST_HUMAN	q8zsd10jx1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE-1853779 3'
80331	20573	33479	0.68	5.8E-01	A1280051.1	EST_HUMAN	q8zsd10jx1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE-1853779 3'
81131	20672	33582	2.34	5.8E-01	P14928	SWISSPROT	SPORE COAT PROTEIN SP96
81131	20672	33583	2.34	5.8E-01	P14928	SWISSPROT	SPORE COAT PROTEIN SP96
88223	21362	34287	9.48	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 8-11
88902	21440	34363	0.89	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
88903	21441	34384	0.50	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
95114	22014		0.89	5.8E-01	BF031606.1	EST_HUMAN	60155774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-3827298 5'
10989	23390	36405	9.44	6.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10915	23434	36601	3.66	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4284403 5'
11021	23535		2.04	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4284403 5'
30779	15694		0.68	5.7E-01	6756253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt), mRNA
32260	15872	28352	1.58	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVOTA)
35552	16156		2.63	5.7E-01	AB033503.1	NT	Populus euphratica leaves-2 mRNA for 1-aminoacyclopropene-1-carboxylate synthases, complete cds
3973	16571	28041	3.09	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (EVGST7*2-BJ1S1) mRNA, partial cds
6498	16087	31881	3.67	5.7E-01	BF035413.1	EST_HUMAN	601454862F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE-3853860 5'
68112	19403	32219	0.72	5.7E-01	AA104201.1	EST_HUMAN	zr38c08.11 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE-985674 5'
68945	16053	30476	1.28	5.7E-01	AL111440.1	NT	Bordetella avium strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.87	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
79111	20453		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kmrl1, Lrp5, Mesh2, Tape-1, Tssc4 and Tssc5 genes, alternative transcripts
87115	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
97115	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22882	35973	0.86	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-40666810 5'
3410	16019	28498	1	5.6E-01	AB016283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	16019	28499	1	5.6E-01	AB016283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	28351	0.69	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
87338	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'

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Table 4

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8738	21277	34201		4.42	5.6E-01 AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9287	21897	34844		1.11	5.6E-01 AB039782.1	NT	Homo sapiens MUC3A gene for intestinal mucus, partial cds
11658	24085			2.5	5.6E-01 BE888280.1	EST_HUMAN	6015140771 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11778	24168	36775		1.28	5.6E-01 AA460335.1	EST_HUMAN	nt_7591051 NCBI_CGAP_Pro Homo sapiens cDNA clone IMAGE:3940874 similar to contains element PTR7 repetitive element;
12158	18028	30490		3.31	5.6E-01 AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12185	24419			2.58	5.6E-01 P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12819	24598			3.11	5.6E-01 BF573829.1	EST_HUMAN	6021320281 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13850	28387		1.13	5.5E-01 6383912	NT	Rattus norvegicus Propriy Coenzyme A carboxylase, beta polypeptide (Pco5), mRNA
2725	15280	27847		13.6	5.5E-01 P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2725	15280	27848		13.6	5.5E-01 P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2943	15559	28033		0.69	5.5E-01 5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S_cerevisiae homolog)-like (SKV2L), mRNA
3102	15717			1.51	5.6E-01 H46210.1	EST_HUMAN	XP_16110.1 Sojae adult brain N25HB557 Homo sapiens cDNA clone IMAGE:175288 5'
3271	15883	28385		2.69	5.6E-01 AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	16358	28825		0.87	5.6E-01 P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8388	20828	33846		0.68	5.6E-01 AJ781768.1	EST_HUMAN	or82011.5 NCBI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9882	22181			0.74	5.6E-01 U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 41585 nucleoprotein gene, complete cds
10279	22774	35763		0.84	5.6E-01 T05047.1	EST_HUMAN	EST02835 Fetal brain, Strategene (cat#036206) Homo sapiens cDNA clone HFBCQ35
151	12814	25301		12.97	5.4E-01 7657288	NT	Homo sapiens KIAA0292 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0292), mRNA
161	12814	25302		12.97	5.4E-01 7657288	NT	Homo sapiens KIAA0292 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0292), mRNA
611	13239	25713		1.6	5.4E-01 AF223208.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
611	13239	25714		1.6	5.4E-01 AF223208.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1314	13808	28428		2.58	5.4E-01 AW886087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NR0040 Homo sapiens cDNA
2154	14731			3.6	5.4E-01 AE002247.2	NT	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome
2286	14870	27446		2.18	5.4E-01 AJ276582.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
3984	16582	28053		0.62	5.4E-01 U07961.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8804 Met protein (M8804 Met) gene, complete cds
6258	17822			1.04	5.4E-01 AW747872.1	EST_HUMAN	QV0-BT0041-0610689-033-e02 BT0041 Homo sapiens cDNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	19239	25713	0.59	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), <i>HrpW</i> (<i>hrpW</i>), and <i>GstA</i> (<i>gstA</i>) genes; complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), <i>HrpW</i> (<i>hrpW</i>), and <i>GstA</i> (<i>gstA</i>) genes; complete cds; and unknown genes
5838	18462	31185	0.81	5.4E-01	AW042327.1	EST_HUMAN	PM2-CR0130-0501200-0039-c10 CN0030 Homo sapiens cDNA
6338	18844	31723	1.49	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7094	18865	32504	1.1	5.4E-01	BE885892.2	EST_HUMAN	6016802768R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39080890 3'
7374	18800	32762	0.75	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7374	18800	32763	0.75	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
							MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-CoA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-CoA DEHYDROGENASE]
7376	19902	32766	1.47	5.4E-01	Q84428	SWISSPROT	
8801	22398		1.88	6.4E-01	BF572236.1	EST_HUMAN	602078545F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243690 5'
10857	23472	36497	3.25	5.4E-01	P36838	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11485	23834	37004	5.79	5.4E-01	Q80675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23834	37005	5.78	5.4E-01	Q80675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11586	18844	31723	2.42	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
11725	24132		2.52	5.4E-01	AI858388.1	EST_HUMAN	w37g04_x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
542	13173	25653	2.28	5.3E-01	AF018413.1	NT	Homo sapiens HLA class III region containing tenascin-X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hemicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
28111	15383	27831	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
28111	15383	27832	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3280	15891	28370	3.13	5.3E-01	AF087588.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4280	16878		1.39	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5949	18277	30753	1.91	5.3E-01	A1820821.1	EST_HUMAN	ZJ42112-y5 Scores every tumor NbHOT Homo sapiens cDNA clone IMAGE:7407115
5949	18277	30754	1.91	5.3E-01	A1820821.1	EST_HUMAN	ZJ42112-y5 Scores every tumor NbHOT Homo sapiens cDNA clone IMAGE:6681125
5742	18388	31075	0.87	5.3E-01	A1A183872.1	EST_HUMAN	ZF22609.1 Scores_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:6681126
5742	18388	31076	0.87	5.3E-01	A1A183872.1	EST_HUMAN	ZF22609.1 Scores_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5827	18451	31174	1.84	5.3E-01	BE845820.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5827	18451	31175	1.84	5.3E-01	BE845820.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

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Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8835	21374			1.83	5.3E-01 L01050.2	NT	Reticula gongenes ribulose 1,5-bisphosphate carboxylase (rbcd) gene, partial cds; chloroplast gene for chloroplast product
8885	21423	34349	0.63	5.3E-01 BF433956.1	EST_HUMAN	7q71c12_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER-29 repetitive element:	7q71c12_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER-29 repetitive element:
8885	21423	34349	0.63	5.3E-01 BF433956.1	EST_HUMAN	WS24b02_x1 NCI_CGAP_Mer15 Homo sapiens cDNA clone IMAGE:2561275 3' similar to SW:COXA_HUMAN_P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;	WS24b02_x1 NCI_CGAP_Mer15 Homo sapiens cDNA clone IMAGE:2561275 3' similar to SW:COXA_HUMAN_P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
10112	22807	35597	0.48	5.3E-01 AI854210.1	EST_HUMAN	W01339867_F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'	W01339867_F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11435	23885	36952	6.92	5.3E-01 BE568291.1	EST_HUMAN	0330405_s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811 APOLIPOPROTEIN D PRECURSOR (HUMAN);	0330405_s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811 APOLIPOPROTEIN D PRECURSOR (HUMAN);
11650	24881		4.22	5.3E-01 AA916053.1	EST_HUMAN	Drosophila melanogaster helix-loop-helix mRNA, complete cds	Drosophila melanogaster helix-loop-helix mRNA, complete cds
849	13465	25973	19.16	5.2E-01 L20770.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1206	13808	28319	10.07	5.2E-01 Q8WV30	SWISSPROT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1223	13832	28348	2.91	5.2E-01 AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds	Homo sapiens phospholipid scramblase 1 gene, complete cds
1830	14514		4.11	5.2E-01 AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens chromosome 21 segment HS21C085
2181	14767	27339	2.97	5.2E-01 AB018263.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds	Homo sapiens mRNA for KIAA0740 protein, partial cds
3163	15767	28233	1.67	5.2E-01 U65942.1	NT	Chlamydomonas reinhardtii S263 POMP91A and POMP90A precursor genes, complete cds	Chlamydomonas reinhardtii S263 POMP91A and POMP90A precursor genes, complete cds
3274	15888		0.71	5.2E-01 D7343.1	NT	Azotobacter vinelandii ldc gene for isocitrate dehydrogenase, complete cds	Azotobacter vinelandii ldc gene for isocitrate dehydrogenase, complete cds
3452	16058		1.74	5.2E-01 AL116780.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
3482	16097	28572	2.49	5.2E-01 AA884165.1	EST_HUMAN	Sm7705_s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'	Sm7705_s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3684	16285		0.92	5.2E-01 AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p11mth) mRNA, nuclear gene encoding chloroplast protein, complete cds	Medicago sativa chloroplast malate dehydrogenase precursor (p11mth) mRNA, nuclear gene encoding chloroplast protein, complete cds
5161	17730		0.87	5.2E-01 AF020269.1	NT	Mus musculus vanilloid receptor-like protein 1 (VH1), mRNA	Mus musculus vanilloid receptor-like protein 1 (VH1), mRNA
5314	17876		0.89	5.2E-01 AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081	Homo sapiens chromosome 21 segment HS21C081
5834	18458	31179	0.97	5.2E-01 AA284261.1	EST_HUMAN	Z044008_77 Scarece_sensecent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'	Z044008_77 Scarece_sensecent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
8846	24795	35115	1.19	5.2E-01 X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
8846	24796	35116	1.19	6.2E-01 X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
8845	22343	35325	0.84	5.2E-01 AA194518.1	EST_HUMAN	Z05508_s1 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE:828783 5'	Z05508_s1 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE:828783 5'
8940	22435	35411	1.85	5.2E-01 AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds	Homo sapiens PELOTA (PELOTA) gene, complete cds
12590	24682		4.94	5.2E-01 P18576	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
845	13288	25746	2.13	5.1E-01 M58508.1	NT	Human adrenodoxin reductase gene, exons 3 to 12	Human adrenodoxin reductase gene, exons 3 to 12
676	13300	25781	3.88	5.1E-01 AJ233944.1	NT	Polyengium vitellinum (strain PI Wt) 16S rRNA gene	Polyengium vitellinum (strain PI Wt) 16S rRNA gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
678	13300	25782	3.98	5.1E-01	AJ233944.1	NT	Polyenolyl vitellinum (strain PI_#1) 16S rRNA gene
1692	14284		0.89	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2068	14049		11.33	5.1E-01	BF883095.1	EST_HUMAN	602138319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:42288117 5'
4151	16745	29197	4.81	5.1E-01	AJ858495.1	EST_HUMAN	WU39512.1 NCI_OGAP_UtI Homo sapiens cDNA clone IMAGE:2427283 3'
4288	16852	28300	3.03	5.1E-01	P86380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5228	17783		0.71	5.1E-01	BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-038 BT0731 Homo sapiens cDNA
6422	19025		0.79	5.1E-01	AV712328	DCA_Homo sapiens cDNA clone DCAAUFO7 5'	AV712328 DCA_Homo sapiens cDNA clone DCAAUFO7 5'
6897	19495	32216	1.42	5.1E-01	R80973.1	EST_HUMAN	Y84609.81 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8507	21046	33986	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0223-180400-172-401 ST0223 Homo sapiens cDNA
8507	21046	33987	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0223-180400-172-401 ST0223 Homo sapiens cDNA
9802	22102	35065	4.8	6.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9803	22103	35068	3.4	5.1E-01	W22202.1	EST_HUMAN	65B1 Human retina cDNA Tsp5081-cleaned sublibrary Homo sapiens cDNA not directional
10085	22580	35555	0.85	5.1E-01	MR4578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	60155883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828787 5'
12128	24385		2.01	5.1E-01	BF438882.1	EST_HUMAN	nae5110.01 NCI_CCap_Bm23 Homo sapiens cDNA clone IMAGE:3405218 3' similar to contains element TAR1 repetitive element :
2180	14757	27328	1.4	5.0E-01	4885552	NT	Homo sapiens postmetiotic segregation Increased 2-like 8 (PMS2L9), mRNA
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmetiotic segregation Increased 2-like 8 (PMS2L9), mRNA
2189	14765	27335	5.48	5.0E-01	AF008210.1	NT	Buchner aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dsbA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gdA) genes, complete cds; and termination factor Rho (rho) gene>
2189	14765	27336	5.46	5.0E-01	AF008210.1	NT	Buchner aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dsbA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gdA) genes, complete cds; and termination factor Rho (rho) gene>
3740	16341	28809	5.58	5.0E-01	AE001785.1	NT	Thermobius maritima section 97 of 135 of the complete genome
38111	18410	28875	0.65	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 3638p_138, partial cds
3842	168540	28908	3.11	5.0E-01	AB023010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8467	21007		1.78	5.0E-01	MR2304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8804	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4043485 3'
8879	20318	33219	3.1	5.0E-01	BF517212.1	EST_HUMAN	601903871F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4136882 5'
9543	22043	35004	1.34	5.0E-01	P35573	SWISSPROT	GLYCOCEN DEBRANCHING ENZYME (GLYCOCEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]							
8543	22043	35005	1.34	5.0E-01	P35573	SWISSPROT	
10281	22788		1.04	5.0E-01	BE989218.1	EST_HUMAN	
11815	24187		3.45	5.0E-01	AF028215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12554	24656		2.38	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12569	24668		4.27	5.0E-01	O13881	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
822	13439	25948	2.31	4.9E-01	BF571462.1	EST_HUMAN	602078648F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1689	14282	20827	1.6	4.8E-01	AJ243855.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1949	14533	27089	1.35	4.8E-01	U40889.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5802	18231	30681	1.32	4.8E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18797	31585	2.35	4.8E-01	AF20831.1	NT	Homo sapiens diacylglycerol kinase 3 (DGAK3) gene, exon 10
6187	18797	31588	2.35	4.8E-01	AF020831.1	NT	Homo sapiens cyclin-dependent kinase 3 (CDK3) gene, exon 10
7475	18997	32882	1.9	4.8E-01	AB04051.1	NT	Oryza sativa subsp. japonica mEF-Q mRNA for mitochondrial elongation factor G, complete cds
8920	21458		1.49	4.8E-01	BF208791.1	EST_HUMAN	601674864F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
						hs80c02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807286 3' similar to TR095714	
9115	21651	34592	0.98	4.8E-01	JW338905.1	EST_HUMAN	TR095714 HERC2.
9220	25126		2.2	4.8E-01	10946883	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13H1), mRNA
10220	22715	35708	0.74	4.8E-01	AF053980.1	NT	Mus musculus adenylyl cyclase 1 (Adcy1) cDNA, partial cds
11704	24117		2.48	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12546	26081		6.73	4.9E-01	AA813582.1	EST_HUMAN	mg22611_s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144652 3'
12553	24957	30872	1.74	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
12630	24708		1.38	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
3591	16196		1.05	4.9E-01	AA912842.1	EST_HUMAN	ab32608_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
4782	17011		0.62	4.9E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5698	18324	30827	8.6	4.9E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6790	18281		4.22	4.8E-01	AA655987.1	EST_HUMAN	nu85f08_s1 NCI CGAP AIM Homo sapiens cDNA clone IMAGE:1217513
7357	18883		1.85	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S228E) mRNA
7682	20174	33081	0.87	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20248	33138	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 4
7738	20248	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 4

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7848	20388	33291	1.38	4.8E-01	AI820744.1	EST_HUMAN	Y77110_5' Scareas breast 2N1HBst1 Homo sapiens cDNA clone IMAGE:154785 5' similar to contains element MER6 repetitive element;
8169	21748		1.13	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
8921	22417	0.58	4.8E-01	BF568833.1	EST_HUMAN	602184287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'	
10607	23141		2.02	4.8E-01	X83502.1	NT	<i>S.cerevisiae</i> ORFs from chromosome X
11788	24170	1.29	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C227 Trypanosoma cruzi transposon V/P II SIRE repeat region	
12016	24842	3.04	4.8E-01	AF227585.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8	
12646	24885	3.38	4.8E-01	AJ132884.1	NT	Q772809_x1 Soares,_testis_NHT Homo sapiens cDNA clone IMAGE:4096387 5'	
68338	19234	32038	8.72	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7107	19447	32263	0.78	4.7E-01	AI204374.1	EST_HUMAN	Q772809_x1 Soares,_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
78036	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
78036	20349	33258	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
9005	21542	34473	0.6	4.7E-01	6881501.1	NT	Rattus norvegicus Sporamine binding protein (Sbp), mRNA
10467	22281	35972	0.79	4.7E-01	AW087781.1	EST_HUMAN	x68911_x1 Scareas_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581580 3'
10727	23253		4.94	4.7E-01	AF102673.1	NT	Influenza A virus isolate Hs1697 hemagglutinin (HA) gene, partial cds
10983	23478	36503	2.19	4.7E-01	U41069.1	NT	Human collagen alpha2(XI)(COL11A2) gene, exons 8 through 16, and partial cds
11163	23570	36715	11.61	4.7E-01	BF528858.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm07 Homo sapiens cDNA clone IMAGE:4181303 5'
11254	23784	36840	2.89	4.7E-01	AW889448.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT00290 Homo sapiens cDNA
11904	24243		1.92	4.7E-01	BE887763.1	EST_HUMAN	60151133SF1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12036	24325		1.33	4.7E-01	AW341561.1	EST_HUMAN	hd11cg8_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'
12888	24738		1.38	4.7E-01	AP000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt, position (777)
3797	16397	28892	2.23	4.6E-01	AW819838.1	EST_HUMAN	RC1-ST0278-040400-018-b08 ST0278 Homo sapiens cDNA
38006	16406	28870	1.68	4.6E-01	BF883300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
38006	16406	28871	1.68	4.6E-01	BF883300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
53223	17885	30390	1.03	4.6E-01	W11287.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
54229	17885	30390	22.08	4.6E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL Na+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCNEG) (GAMMA NACH)
5440	17885	30400	1.37	4.6E-01	P51170	SWISSPROT	
56112	18241	30690	1.12	4.6E-01	BF513583.1	EST_HUMAN	601800234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
66112	18241	30691	1.12	4.6E-01	BF513583.1	EST_HUMAN	601800234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
56633	18280	30798	3.27	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
56633	18280	30789	3.27	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18361	31067	2.38	4.6E-01	BE734781.1	EST_HUMAN	601568765F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.8E-01	AI247078.1	EST_HUMAN	ch58102_x1 Soares_fetal_liver_spiken_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O15338 O15338 BUTYROPHILIN.
5748	18374	31083	4.22	4.8E-01	AI247078.1	EST_HUMAN	ch58102_x1 Soares_fetal_liver_spiken_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O15338 O15338 BUTYROPHILIN.
5759	18382	31094	1.4	4.8E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18452		1.05	4.8E-01	AF212124.1	NT	Anolis schwartz cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5907	18529		0.88	4.8E-01	BE817247.1	EST_HUMAN	PMD-BN0280-120600-001-F07 BN0280 Homo sapiens cDNA
6058	18875	31417	0.75	4.8E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6404	19007	31788	1.05	4.8E-01	AE000894.1	NT	Methanococcinum thermophilicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6885	19589	32429	1.38	4.8E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6885	19589	32430	1.38	4.8E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.88	4.8E-01	AA483577.1	EST_HUMAN	nh04h05_s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element contains element L1 repetitive element :
8282	20803	33721	13.23	4.8E-01	BF897398.1	EST_HUMAN	60213086851 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:42878285
9225	21741	34684	1.04	4.8E-01	P552022	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.8E-01	P552022	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9583	22083	35046	0.55	4.8E-01	AF162263.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.8E-01	AF162263.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22383	35398	2.63	4.8E-01	AI915834.1	EST_HUMAN	wg73612_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9886	22383	35398	2.63	4.8E-01	AI915834.1	EST_HUMAN	wg73612_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10870	23391		3.09	4.8E-01	P081163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (1_L)
10870	23400	38416	4.13	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-905 HT0730 Homo sapiens cDNA
10870	23400	38417	4.13	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-076-905 HT0730 Homo sapiens cDNA
11346	23044	38054	5.52	4.8E-01	AF018368.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	38055	5.52	4.8E-01	AF018369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12854	24728		1.28	4.8E-01	M222360.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants &I, 12J, 13J, and 17J mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954 14538	27094		1.89	4.5E-01	AE001931.1	NT	Danio rerio nucleic acids R1 section 88 of 228 of the complete chromosome 1
1954 14538	27095		1.89	4.5E-01	AE001931.1	NT	Danio rerio nucleic acids R1 section 88 of 228 of the complete chromosome 1
2895 15512	27882		4.77	4.5E-01	AA877088.1	EST_HUMAN	255d02_s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4541783' xc25c08.x1 NCI_CGAP_Ox18 Homo sapiens cDNA clone IMAGE:2585280 3' similar to gb:107807
3348 15958	28431		0.84	4.5E-01	AW083761.1	EST_HUMAN	DYNAMIN-1 (HUMAN); DYNAMIN-1 (HUMAN);
3348 15958	28432		0.84	4.5E-01	AW083761.1	EST_HUMAN	xc25c08.x1 NCI_CGAP_Ox18 Homo sapiens cDNA clone IMAGE:2585280 3' similar to gb:107807
3359 15967	28444		5.16	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3424 16032	28512		1.15	4.5E-01	AF128378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4100 16684			1.35	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4149 16741	28785		0.73	4.5E-01	AI708808.1	EST_HUMAN	ss98e09.x1 Barreto et al. HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4225 18015			4.04	4.5E-01	AW873495.1	EST_HUMAN	ho80g02.x1 Scores_NFL_T_GBC_91 Homo sapiens cDNA clone IMAGE:3041810 3'
5078 17651	30092		1.16	4.5E-01	BE863445.2	EST_HUMAN	601657223R1 NH_MGC_67 Homo sapiens cDNA clone IMAGE:3868023 3'
5427 17984			26.74	4.5E-01	AF060106.1	NT	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
5737 18363	31070		1.37	4.5E-01	AW808814.1	EST_HUMAN	QV2_PFT0012-140100-031-c09_PT0012 Homo sapiens cDNA
6718 18313			1.36	4.5E-01	Q009856	SWISSPROT	COAT PROTEIN
7443 18887	32834		1.89	4.5E-01	M37036.1	NT	Rat nuclear proteins B23.1 and B23.2
7604 20117	32883		2.53	4.5E-01	AI858849.1	EST_HUMAN	w32e02.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR_Q92923 Q92923 SW_ISNF COMPLEX 170 KDA SUBUNIT.;
8248 20790			0.97	4.5E-01	M32881.1	NT	D melanogaster Shaw2 protein mRNA, complete cds
8342 20883	33804		4.02	4.5E-01	AI848598.1	EST_HUMAN	tc28g11.x1 NCI_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2282844 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8484 21033	33954		0.89	4.5E-01	Q52728	SWISSPROT	Homo sapiens hypothetical protein DKF4p47G153 (DKF4p47G153), mRNA
8716 21255			1.74	4.5E-01	11444788	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
8828 21467	34385		0.88	4.5E-01	AE000218.1	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
9853 22251			1.02	4.5E-01	9830816	NT	EST02531 Fetal brain, Stratagene (cat#636205) Homo sapiens cDNA clone HFBCY17
10389 22883	35877		23.95	4.5E-01	MB8008.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#636205) Homo sapiens cDNA clone HFBCY17
10389 22883	35878		23.95	4.5E-01	MB8008.1	EST_HUMAN	xp14h01.x1 NCI_CGAP_UG Homo sapiens cDNA clone IMAGE:2703885 3' similar to SW:INT8_MOUSE
10744 23268	36285		3.01	4.5E-01	AW591271.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-8. [1];
11131 23659			1.9	4.5E-01	AV718382.1	EST_HUMAN	AV718382 GLC Homo sapiens cDNA clone GLCCED125'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23828	36890	1.68	4.5E-01	BE068472.1	EST_HUMAN	RC3-BT0333-160300-016-003 BT0333 Homo sapiens cDNA
11871	25070		3.3	4.5E-01	BE871461.1	EST_HUMAN	601448201F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3852881 5'
12370	24540		2.13	4.5E-01	BF327511.1	EST_HUMAN	602035275F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183280 5'
12442	24578		6.25	4.5E-01	11422089	NT	Homo sapiens testis-specific kinase 2 (TESTK2). mRNA
2081	14882		1.39	4.4E-01	0880503	NT	<i>Mus musculus integrin membrane-associated protein 1 (Imap1). mRNA</i>
2432	14989	27572	3.26	4.4E-01	P40785	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3357	15985	28442	1.27	4.4E-01	AF058780.1	NT	<i>Rattus norvegicus SynGAP-b mRNA, complete cds</i>
3357	15985	28443	1.27	4.4E-01	AF058780.1	NT	<i>Rattus norvegicus SynGAP-b mRNA, complete cds</i>
3381	15989	28446	2.31	4.4E-01	BF056728.1	EST_HUMAN	7191602.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3383795 5'
4318	16804		1.28	4.4E-01	BE378707.1	EST_HUMAN	601237138F1 NIH_M3C_44 Homo sapiens cDNA clone IMAGE:36008383 5'
5134	17706		2.07	4.4E-01	BE141388.1	EST_HUMAN	MRD-HT078-131289-007-005 HT0078 Homo sapiens cDNA
5277	17839	30285	0.94	4.4E-01	U61154.1	NT	Bizura suppressaria nucleopolyhedrovirus ecdisystroid UDP-glucosyltransferase (sgt) gene, complete cds
5417	17874		0.9	4.4E-01	AW614685.1	EST_HUMAN	MR1-ST0208-120400-022-007 ST0208 Homo sapiens cDNA
5613	18212	30682	4.06	4.4E-01	PO4628	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18212	30683	4.06	4.4E-01	PO4628	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5887	18489	31215	1.72	4.4E-01	S65019.1	NT	<i>musca (Musca) Sprague-Dawley, sulfur-diode-treated tracheal epithelium, mRNA Partial, 390 nt</i>
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6108	18724	31476	1.53	4.4E-01	AI198413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1881125 3' similar to TR:Q29168 Q29168
6108	18724	31477	1.53	4.4E-01	AI198413.1	EST_HUMAN	UNKNOWN PROTEIN;
6387	18890	31771	1.69	4.4E-01	AW6080785.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1881125 3' similar to TR:Q29168 Q29168
6470	19071		1.02	4.4E-01	AA776132.1	EST_HUMAN	aa85d11.61 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970895 3' similar to gbm16038
7429	19853	32813	0.89	4.4E-01	AE000571.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN); Halobacter pylori 28836 section 49 of 134 of the complete genome
7782	20325		10.05	4.4E-01	Z11679.1	NT	<i>S. tuberosum mRNA for induced statin lip protein (partial)</i>
8888	21237	34160	1.01	4.4E-01	AA058427.1	EST_HUMAN	2f08ea03.s1 Stratagene cDNA clone IMAGE:5038386 3'
9078	21614	34549	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 081074 from USA, envelope glycoprotein (env) gene, partial cds
9111	21647	34587	0.58	4.4E-01	AW612578.1	EST_HUMAN	hh05c08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to
9214	21731	34674	1.13	4.4E-01	O62836	SWISSPROT	<i>SW_MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6; ZINC FINGER X-CHROMOSOMAL PROTEIN</i>

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	22369	36347	1.69	4.E-01	AI268850.1	EST_HUMAN	q33979.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910821 3'
8873	22370		2.12	4.E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35405	4.51	4.E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10276	22771	35758	1.43	4.E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Goronti, 8883 nt, segment 2 of 2]
10276	22771	35760	1.43	4.E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Goronti, 8883 nt, segment 2 of 2]
11839	24271	31016	4.68	4.E-01	6877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn1ba), mRNA
11952	25000		14.98	4.E-01	AL163222.2	NT	Homo sapiens chromosome 21 segment HS21/C082
12517	24635		1.5	4.E-01	P34725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
4383	13069	25564	1.77	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
4383	13069	25565	1.77	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
30983	15711	28182	0.91	4.3E-01	AW989477.1	EST_HUMAN	MRD-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	16819	28208	1.21	4.3E-01	J00306.1	NT	Human somatosatin 1 gene and flanks
4495	13069	25564	3.86	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13069	25565	3.86	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
5507	18188	30845	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5507	18188	30846	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18868	31407	1.34	4.3E-01	BE181655.1	EST_HUMAN	QV-HT0838-070500-181-d08 HT0838 Homo sapiens cDNA
6035	18862	31424	2.06	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6809	19400	32215	4.28	4.3E-01	AJ001678.1	NT	Catolmis columnis japonica fmg3 gene
6949	19526		0.78	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7459	19880		1.78	4.3E-01	BF348001.1	EST_HUMAN	602023134f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158298 5'
8386	20906		2.66	4.3E-01	U97040.1	NT	Mathanococcus velutae flagella-related protein C1 (fslC-fsl) genes, complete cds
9179	21753	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsA gene
9842	22142	35108	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh746f10.y1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:2688554 5'
9842	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	xn63a05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688554 5'
10128	22682	35814	0.57	4.3E-01	AW170559.1	EST_HUMAN	TR:0001189 0001189 Mu-ADAPTIN RELATED PROTEIN 2 :
10811	19816	32451	2.62	4.3E-01	AF075829.1	NT	Equus caballus microsatellite LE0277
11588	24031	37101	1.54	4.3E-01	AI87432.1	EST_HUMAN	128-404.x1 NCI_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:22833351 3'
11632	18198	30845	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
11632	18198	30846	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12816	24689		2.81	4.3E-01	AJ003022.1	NT	Streptomyces costicola wh1 gene
1402	15440	26524	1.39	4.2E-01	Q38102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1891	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288868 3'

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20988	14846			1.37	4.2E-01 AF258325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
36869	16270	28738	4.91	4.2E-01 AE003847.1	NT	Xylella fastidiosa, section 83 of 229 of the complete genome	
36869	16300	28768	1	4.2E-01 AI280338.1	EST_HUMAN	qb4801.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'	
3773	18914		0.6	4.2E-01 NB12031.1	EST_HUMAN	7881E1 fetal brain cDNA Homo sapiens cDNA clone 7881E1-K similar to R07879, Z40498	
39448	16546	28014	0.73	4.2E-01 AW835257.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA	
40554	16851	28118	0.88	4.2E-01 Q048883	SWISSPROT	SOX-8 PROTEIN	
4807	17985	28835	4.3	4.2E-01 AA534083.1	EST_HUMAN	nr89h01.s1 NCI_OGAP_Pt10 Homo sapiens cDNA clone IMAGE:3977777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN)	
48895	17470	28926	4.04	4.2E-01 R13467.1	EST_HUMAN	yf77e01.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:28278 5'	
52232	17798		3.77	4.2E-01 U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds	
56891	18514	31241	1.52	4.2E-01 BF242055.1	EST_HUMAN	60187971F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'	
56553	18575	31309	2.16	4.2E-01 AW854162.1	EST_HUMAN	RC3-C10254-080400-028-904 CT0254 Homo sapiens cDNA	
68552	18857	31738	1.06	4.2E-01 AL169247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
7031	19565	32392	10.28	4.2E-01 AU158472.1	EST_HUMAN	AU158472 PLACE22 Homo sapiens cDNA clone PLACE20000470 3'	
7031	19565	32383	10.28	4.2E-01 AU158472.1	EST_HUMAN	AU158472 PLACE22 Homo sapiens cDNA clone PLACE20000470 3'	
7082	24776	32492	1.97	4.2E-01 S82504.1	NT	Brazil-breast cancer gene [rats, WF, spleen, Gernetic, 419 nt, segment 2 of 2]	
7150	18883	32524	5.81	4.2E-01 AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47	
7834	20476	33385	2.61	4.2E-01 AW857448.1	EST_HUMAN	EST389413 MAGE sequences, MAGE_Homo sapiens cDNA	
7834	20476	33388	2.61	4.2E-01 AW857448.1	EST_HUMAN	EST389413 MAGE sequences, MAGE_Homo sapiens cDNA	
8148	20889	33602	0.55	4.2E-01 4758039 NT	mRNA	Homo sapiens cytochrome c oxidase subunit Vtc (COX6C), nuclear gene encoding mitochondrial protein,	
92335	21761	34708	0.52	4.2E-01 U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds	
92335	21761	34707	0.52	4.2E-01 U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds	
98880	22377		0.81	4.2E-01 AA705007.1	EST_HUMAN	4f8f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:402849 3'	
10083	22518	35571	0.5	4.2E-01 AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds	
10390	22884	35870	1.35	4.2E-01 AW863886.1	EST_HUMAN	MR3-SN010-280300-102-107 SN01010 Homo sapiens cDNA	
10821	23440	38461	3.68	4.2E-01 ABC023489.1	NT	Oryzias latipes OKGC7 mRNA for membrane gamma1 cyclase, complete cds	
11273	23128	36780	2.65	4.2E-01 BE986485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3900085 3'	
12561	24681		1.49	4.2E-01 AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'	
1133	13736	28245	1.59	4.1E-01 A1805481.1	EST_HUMAN	RC-BT09-1-210189-142 BT091 Homo sapiens cDNA	
1142	13745	28254	1.54	4.1E-01 AV705243.1	EST_HUMAN	AV705243 ADB_Homo sapiens cDNA clone ADBAHF08 5'	
1142	13745	28255	1.54	4.1E-01 AV705243.1	EST_HUMAN	AV705243 ADB_Homo sapiens cDNA clone ADBAHF08 5'	
2735	15280	27858	1.58	4.1E-01 7705283 NT	mRNA	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA	
2867	15582	28061	2.11	4.1E-01 AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38	

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2887	15682	28082	2.11	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 38
3342	15682	28428	0.98	4.1E-01	AA696344.1	EST_HUMAN	GB4b08.81 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE11605843 3'
3839	18438	28889	0.58	4.1E-01	AW981292.1	EST_HUMAN	EST373384 MAGE sequences, MAGG Homo sapiens cDNA
3839	18438	28900	0.58	4.1E-01	AW981292.1	EST_HUMAN	EST373384 MAGE sequences, MAGG Homo sapiens cDNA
4381	16948	28390	2.32	4.1E-01	AJ2492207.1	NT	Rhodococcus sp. AD45 isoC, isoH, isoL, isoM, isoA, isoB, isoC, isoD, isoE and isoF genes
4383	16979		0.70	4.1E-01	AA6909257.1	EST_HUMAN	cmt3d02.61 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE11642819 3'
4774	17355	28607	1.31	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NP0CBDF10 5'
6141	18755	31513	3.97	4.1E-01	BF581363.1	EST_HUMAN	60211565801 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4287319 5'
7480	19883	32848	2.74	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7979	20521	33427	1.31	4.1E-01	BF574684.1	EST_HUMAN	602113326171 NIH_MGC_81 Homo sapiens cDNA clone IMAGE4288238 5'
8019	21556	34484	1.26	4.1E-01	0755621	NT	<i>Mus musculus</i> signaling intermediate in Tcf1 pathway-evolutionarily conserved (Sipep-pending), mRNA
9484	21941		0.61	4.1E-01	AF-60507.1	NT	Vaeleto gymnoceatus Vgpm580 cytochrome b (cyt b) gene, complete cds; mitochondrial gene for mitochondrial product
10164	22859		1.26	4.1E-01	AL138078.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 3/8
10310	22804	35798	0.79	4.1E-01	AV649579	GLC Homo sapiens cDNA clone GLC3V0D12 3'	
10401	22885	35890	0.51	4.1E-01	P18584	SWISSPROT PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 kDa IMMUNOGENIC PROTEIN) (SK59)	
10401	22885	35891	0.51	4.1E-01	P18584	SWISSPROT PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 kDa IMMUNOGENIC PROTEIN) (SK59)	
10471	22865		2.20	4.1E-01	BF5349282.1	EST_HUMAN	CMP2-HT0137-200909-010-008 HT0137 Homo sapiens cDNA
10719	23247	36282	45.22	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zeta protein
11270	23008	36015	3.57	4.1E-01	Q98470	SWISSPROT VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HVK1)	
12280	25049		2.6	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
147	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-200609-012-d10 CT0201 Homo sapiens cDNA
1077	13581	26191	0.82	4.0E-01	8404656	NT	Lequeus rubellus mitochondrial, complete genome
1394	13978	26505	1.81	4.0E-01	AF203478.1	NT	Drosophila melanogaster Deltation (dmt) mRNA, complete cds
1532	14124		4.1	4.0E-01	68769258	NT	<i>Mus musculus</i> platelet derived growth factor receptor, beta polypeptide (Pdgfb), mRNA
2049	15456	27200	1.22	4.0E-01	2868633.1	NT	<i>Ascaris lumbricoides</i> massc2 gene
2049	15456	27201	1.22	4.0E-01	2868633.1	NT	<i>Ascaris lumbricoides</i> massc2 gene
2204	14780	27352	17.82	4.0E-01	AE001821.1	NT	<i>Deinococcus radiodurans</i> R1 section 68 of 220 of the complete chromosome 1
2204	14780	27353	17.82	4.0E-01	AE001821.1	NT	<i>Deinococcus radiodurans</i> R1 section 68 of 220 of the complete chromosome 1
2381	12811	25389	1.45	4.0E-01	6878490	NT	<i>Mus musculus</i> ubiquitin-protein ligase a3 component n-recognin (Ubr1), mRNA
2385	15811	28090	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2386	15611	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	18359	28829	2.17	4.0E-01	AF088803.1	NT	Streptococcus pneumoniae YIC (YIC), YID (YID), penicillin-binding protein 2x (pbp-2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide transferase (mraY) genes, complete cds
38898	18498	28860	3.04	4.0E-01	AJ277511.1	NT	Ovs arises partial JD2 gene for T cell receptor delta chain (TCRD12), exon 1
38899	18498	28861	3.04	4.0E-01	AJ277511.1	NT	Ovs arises partial JD2 gene for T cell receptor delta chain (TCRD12), exon 1
4842	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
50059	18858	31429	1.16	4.0E-01	AW970810.1	EST_HUMAN	EST382891 IMAGE: sequences, MAGK Homo sapiens cDNA STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E1, E2 AND E1; 6 KD PEPTIDE]
65607	19165	31981	0.87	4.0E-01	P27285	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
77777	20286	33183	0.72	4.0E-01	P27548	SWISSPROT	EST_HUMAN
78689	20411	33317	0.46	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA EST26068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alt repeat
79554	20498	33406	0.99	4.0E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
88336	21474	34394	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST26068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alt repeat
11443	23883		1.65	4.0E-01	BF030232.1	EST_HUMAN	801558283F1 NIH MGC_58 Homo sapiens cDNA clone IMAGE:3828902 5'
11568	24015		3.52	4.0E-01	L75080.1	NT	Synecochrysins sp. PCGC 9413 transposase gene, complete cds
11958	24901		2.5	4.0E-01	AL168330.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	246348		1.42	4.0E-01	P38049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2 STE3 INTERGENIC REGION
1420	14013	26543	1.98	3.8E-01	AF206816.1	NT	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2688	15220	27798	3.8	3.8E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2730	15295	27851	3.79	3.8E-01	X82032.1	NT	H. sapiens B-myb gene
2730	15285	27852	3.79	3.8E-01	X82032.1	NT	H. sapiens B-myb gene
3131	15745	28214	3.85	3.8E-01	AJ225896.1	NT	Short tandem motif (stf) syB2, cys3 genes and orf3
41153	16745	28198	1.49	3.8E-01	BF582611.1	EST_HUMAN	7616d01.x1 NC1_CGAP_Br18 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30138	1.88	3.8E-01	BE729897.1	EST_HUMAN	601563848F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3833888 5'
60890	18708	31454	6.44	3.8E-01	BF209036.1	EST_HUMAN	601862382F1 NIH MGC_53 Homo sapiens cDNA clone IMAGE:4155322 5'
6428	19029	31812	0.68	3.8E-01	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28S7S protein (XQ28ORFY), and biglycan (BCN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7886	20438	33343	0.78	3.8E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-1) gene, complete cds
8785	21334	34259	0.73	3.8E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170889-004-608 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.8E-01	BF348634.1	EST_HUMAN	602018944F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155322 5'
9161	21586	34840	1.24	3.8E-01	AW195898.1	EST_HUMAN	xn86d04.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:0p4821
							0p4821 KIAA0713 PROTEIN;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21989	34945	1.42	3.9E-01	A1837337.1	EST_HUMAN	wp78602.11 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW-FXFX5_HUMAN P48362 BINDING REGULATORY FACTOR ;
9792	22290	35274	3.68	3.9E-01	M19879.1	NT	Human clathrin 27 gene, exons 10 and 11, and L1 and Alu repeats
9858	22354		0.5	3.9E-01	11485620	NT	Porphyra purpurea mitochondrion, complete genome
10071	22568	35561	0.69	3.9E-01	D88722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10482	22898	35693	0.46	3.9E-01	M18440.1	NT	Human beta-R2-crystallin (B2-1) gene, exon 4, partial cds
10700	23229		1.82	3.9E-01	AV686874.1	EST_HUMAN	AV686874 GKC Homo sapiens cDNA clone GKCBQC115'
11728	24977		3.42	3.9E-01	AF504354.1	NT	Homo sapiens proteophagen 3 (PRGS) gene, complete cds
11854	24214		1.42	3.9E-01	Q61670	SWISSPROT	HOMEBOX PROTEIN Hlx1
11930	24268	31015	1.56	3.9E-01	AE001811.1	NT	Thermodoga maritima section 123 of 138 of the complete genome
12389	24551		1.37	3.9E-01	11433395	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583). mRNA
171	12834		19.28	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (p110beta), mRNA
531	13182		3.11	3.8E-01	AB028281.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1011	14489		0.69	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 228 of the complete genome
20015	15167	27734	1.89	3.8E-01	AF214117.1	NT	Archidiopsis freiliana putative c-myc-like transcription factor (M1YCR-3) mRNA, complete cds
2861	15473	27781	3.04	3.8E-01	8878002	NT	Mus musculus scute carrier family 1, member 6 (Sic160), mRNA
3034	15650		0.89	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)
3084	15859	28173	2.2	3.8E-01	AF043383.1	NT	Pleuroneurodes americanus arninopeptidase N (arnpN) gene, partial cds
35330	16126	28815	9.83	3.8E-01	AL161518.2	NT	Archidiopsis thailandica DNA chromosome 4, config fragment No. 30
3592	16168		0.59	3.8E-01	AB07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3609	16186		0.75	3.8E-01	AB07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3620	16420	28882	0.94	3.8E-01	BE154030.1	EST_HUMAN	PM0-H-TG339-200400-010-C01 HT0339 Homo sapiens cDNA
3699	16597	29058	0.8	3.8E-01	9754095	NT	Mus musculus general transcription factor II I (GTF2I), mRNA
4138	16730	29183	0.99	3.8E-01	AJ271361.2	NT	Tetragyu rubripes wrt2 (partial), frank1, crt and frak2 (partial) genes
5271	17853	30258	0.89	3.8E-01	BE544653.1	EST_HUMAN	601074110f1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							yr88a11.7 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:210428 5' similar to ob146703HUMAALL34 Human carcinoma cell-derived Alu RNA transcript, (RNA); gb:AA863566
							EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN) contains Alu repetitive element; element contains MER4 repetitive element;
5412	17889	30378	1.07	3.8E-01	H64927.1	EST_HUMAN	TRANSCRIPTION FACTOR SOX-10
5794	18419	31135	1.11	3.8E-01	Q04888	SWISSPROT	protein protein [link, Germline, 2446 nt]
6481	18082		0.68	3.8E-01	S48825.1	NT	OV2-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6737	19331	32137	5.29	3.8E-01	BE072390.1	EST_HUMAN	ts54f11.x1 Soares_total_fetus_Nb21F8_8w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element,
6857	19591	32423	3.97	3.8E-01	A137401.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32239		1.33	3.8E-01 AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 25
76265	20045			4.75	3.8E-01 X61587.1	NT	N. musculus gene for klf10/reln-binding protein
82238	20779	33700		0.49	3.8E-01 M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
84922	21031	33951		2.34	3.8E-01 AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
85580	21089	34019		1.14	3.8E-01 11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1) mRNA
87751	21280	34210		1.12	3.8E-01 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9480	21879			4.03	3.8E-01 T05413.1	EST_HUMAN	yel4h08.1 Scarece fetal liver spleen cDNA clone IMAGE:120539 5' similar to contains
11408	23859			3.5	3.8E-01 BE718218.1	EST_HUMAN	Alu repetitive element; contains PTTR5 repetitive element;
11541	23889	37080		2.95	3.8E-01 R42550.1	EST_HUMAN	RC04-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11541	23889	37081		2.95	3.8E-01 R42550.1	EST_HUMAN	yf22h11.51 Scarece infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272			2.81	3.8E-01 AE001124.1	NT	yf22h11.51 Scarece infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12058	24888			1.75	3.8E-01 UB4788.1	NT	Bornella burgdorferi (section 10 of 70) of the complete genome
12180	24421			1.45	3.8E-01 BE828258.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
12565	24684			2.22	3.8E-01 U78031.1	NT	QV3-ET0063-190700-271-a25 ET0063 Homo sapiens cDNA
12638	24713	30896		1.25	3.8E-01 AF194972.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
2521	15085	27857		15.01	3.7E-01 AB937831.1	NT	Mus musculus developmental control protein mRNA, partial cds
3507	16112	28589		10.94	3.7E-01 AF056398.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3838	16538	28003		0.88	3.7E-01 AA319482.1	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4313	16889	28344		9.19	3.7E-01 AI218707.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA clone IMAGE:1510188 3'
4412	16987	29440		1.18	3.7E-01 AW870337.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4479	17084	28514		3.13	3.7E-01 AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5838	18557	31285		1.27	3.7E-01 AF135187.1	NT	Homo sapiens interferon-induced protein p78 (Mx1) gene, complete cds
6105	18721	31474		0.94	3.7E-01 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6633	19229	32033		1	3.7E-01 M10806.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
68851	19247			0.81	3.7E-01 L10353.1	NT	Mus musculus haptoglobin mRNA, complete cds
7197	19728	32570		4.44	3.7E-01 11625843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA
8271	20812	33733		1.88	3.7E-01 11439739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12orf4) mRNA
8271	20812	33734		1.88	3.7E-01 11439739	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
8306	20847	33770		0.78	3.7E-01 AA802912.1	EST_HUMAN	ck3b11.51 NCI_CGAP_Lef2 Homo sapiens cDNA clone IMAGE:1516701 3'
91289	21684			1.54	3.7E-01 AJ271988.1	NT	Gelius gene mRNA for beta-carotene 15,15'-dioxygenase (BCDO gene)
10074	22589			0.48	3.7E-01 K00691.1	NT	mouse Ig gamine alpha membrane exons region
10111	22608	35588		4.17	3.7E-01 AI338411.1	EST_HUMAN	q46b07>1 Scarece fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1850987 3'
10809	23428	38446		3.47	3.7E-01 A1297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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10909	23428	38447	3.47	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36049	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11549	23907		1.6	3.7E-01	AA973540.1	EST HUMAN	co48d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1589221 3' similar to gb:M77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
11603	24048		2.78	3.7E-01	6877878	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11640	24601		1.82	3.7E-01	J04882.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas psittaci partial cyp1 gene for outer membrane protein 1
11913	24251		4.72	3.7E-01	D88978.1	NT	Human mRNA for KIAA0223 gene, partial cds
12302	24489		2.84	3.7E-01	AL121154.1	EST HUMAN	DKFZp762k075_j1_782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762k075_5'
12377	24545		7.01	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
12822	12839	25424	1.07	3.8E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1033	13043		8.45	3.8E-01	U89241.1	NT	Human mmp8 gene, partial cds
1357	13851	28477	4.32	3.8E-01	T80255.1	EST HUMAN	ye03405.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443_5'
1357	13951	28478	4.32	3.8E-01	T80256.1	EST HUMAN	ye03405.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443_5'
1859	14543	27059	6.39	3.8E-01	IAW580184.1	EST HUMAN	hg3302.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419_3'
1859	14543	27100	6.39	3.8E-01	IAW580184.1	EST HUMAN	hg3302.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419_3'
1884	14578	27138	7.23	3.8E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2088	14877		0.88	3.8E-01	AF056827.1	NT	Rattus norvegicus repeat element associated with the Rassgrf1 gene
2309	14881		1.13	3.8E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2433	15000		2.49	3.8E-01	X78725.1	NT	Pinegrilase (P3804) gene for actin
2528	15082	27665	3.34	3.8E-01	AW812033.1	EST HUMAN	RC5-ST0171-181088-01-007 S10171 Homo sapiens cDNA
							(PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN-L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE))
2859	15218	27789	1.38	3.8E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sub3) mRNA, complete cds
2824	18012		10.38	3.8E-01	AF188448.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3518	16121	28600	2.16	3.8E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3518	16121	28601	2.16	3.8E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4497	17081	28530	1.97	3.8E-01	BE70783.1	EST HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4850	17428	28880	0.94	3.8E-01	AJ009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4887	17443	28884	0.65	3.8E-01	Y11528.1	NT	Zmays mRNA for cassein kinase II alpha subunit
5153	17723	30154	2.28	3.8E-01	AW338893.1	EST HUMAN	hg02904.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872588_3'
5261	17824	30249	0.58	3.8E-01	BE087689.1	EST HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6236	18845	31616	1.16	3.8E-01	P16431	SWISSPROT	FORMATTE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6804	19201	32006	1.68	3.6E-01	Y10186.1	NT	Homo sapiens PHEX gene
7202	19733		4.57	3.6E-01	RS4090.1	EST_HUMAN	Y74608.1 1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5' W72c10.1 1 Scares_thymus_NHFTH Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7327	18854	32717	1.73	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1]; SCOPROTEIN
8168	20707	33623	0.68	3.6E-01	P08167	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8221	20702	33676	13.59	3.6E-01	AL101583.2	NT	
8392	21470	34388	3.08	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8392	21470	34389	3.08	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	216593	34597	1.32	3.6E-01	AL103204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9320	21834	34784	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9390	21813		0.54	3.6E-01	X62825.1	NT	C-perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
9777	222775	35260	16.15	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9804	22401	35374	0.53	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211088-002-b10 CT0222 Homo sapiens cDNA
9804	22401	35376	0.53	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211088-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.6E-01	BE802280.1	EST_HUMAN	601678418F-1 NIH_ MGCC_21 Homo sapiens cDNA clone IMAGE:3958897 5'
10987	23501	36531	4.15	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SipB3, complete cds
11065	23577	36615	2.02	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
11318	23018	36025	4.07	3.6E-01	AE000896.1	NT	Methanobacterium thermosulfidophilum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11680	25109		2.45	3.6E-01	Y19210.1	NT	Homo sapiens Hh1b5 gene for hair keratin, exons 1 to 9
11788	24199		5.79	3.6E-01	AE000395.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11923	24293		4.7	3.6E-01	U68888.1	NT	Mus musculus Ensr1 mRNA, complete cds
12308	24502		2.18	3.6E-01	114325988	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (frithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
120	12791	25273	1.35	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
223	12804	25369	2.67	3.5E-01	6678833	NT	Mus musculus mRNA receptor, C type 2 (Mrc2), mRNA
706	13327	26814	4.48	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
754	13373	25988	1.39	3.5E-01	7700136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
754	13373	25989	1.39	3.5E-01	7700136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
812	13430	25835	3.83	3.5E-01	BF128788.1	EST_HUMAN	601610050R1 NIH_MGCC_48 Homo sapiens cDNA clone IMAGE:4053861 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	14274	26807	1.91	3.5E-01	U35778.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14893	27469	1.12	3.5E-01	P06788	SWISSPROT	HOMEBOX PROTEIN HOXA-4 (HOX-1.4) (MH-3)
2837	15472	27770	1.92	3.5E-01	AA223262.1	EST_HUMAN	zr08a09.s1 Strategene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:6508723'
2729	15284	28124	11.8	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3030	15846	28124	0.57	3.5E-01	AA057691.1	EST_HUMAN	ZB94f03.71 Strategene corneal stroma (#837222) Homo sapiens cDNA clone IMAGE:5122855'
3873	16473		1.27	3.5E-01	AA042138.1	EST_HUMAN	nr06003.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:11723573'
4349	16836	28377	2.3	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxa5b) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	7581E1 fetal brain cDNA Homo sapiens cDNA clone 7881E1-K similar to R07879, Z40498
5088	17639	30052	4.33	3.5E-01	M16348.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5537	18169	30583	0.74	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5537	18169	30584	0.74	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5738	18364	31071	1.42	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6384	18988		0.9	3.5E-01	AW883916.1	EST_HUMAN	PM4-SN012430400-001-411 SN01212 Homo sapiens cDNA zv78f03.r1 Scores_tests_NtT Homo sapiens cDNA clone IMAGE:7824285 similar to TR: 1088835
6540	19139	31982	0.75	3.5E-01	AA431833.1	EST_HUMAN	G1006836 F10F2.1;
6578	19176	31976	0.72	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfide reductase (mtsA) mRNA, complete cds
6770	19363	32172	0.93	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7116	19458		3.51	3.5E-01	X88805.1	NT	S. cerevisiae mRNA for CD31 protein (PECAM-1)
8016	20558		2.02	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8019	20561	33462	0.65	3.5E-01	BF358871.1	EST_HUMAN	RC4-ET0024-2650800-014-d07 ET0024 Homo sapiens cDNA
8403	20943		0.61	3.5E-01	AF051681.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nicc1) mRNA, complete cds
8857	21386	34319	1.12	3.5E-01	4507810	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9851	22150	35120	1.83	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII)
9801	22289	35284	4.91	3.5E-01	Z26825.1	NT	X. laevis gene for albumin including H1P1 enhancer
9877	22374	35351	1.14	3.5E-01	BE177794.1	EST_HUMAN	QV2-HT0577-000400-128-c07 HT0577 Homo sapiens cDNA
10613	23148	38157	4	3.5E-01	X61084.1	NT	C. griseus rhodopsin gene for opsin protein
10802	23422	38440	2.08	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10802	23422	38441	2.08	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11462	23912	38879	1.83	3.5E-01	N77597.1	EST_HUMAN	y200t12r1 Scores_multiple_scorerases_2NbH-MSP Homo sapiens cDNA clone IMAGE:28033755'
11532	23980	37050	1.71	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	25112			1.51	3.5E-01 AF297468.1	NT	Schistosoma mansoni strain NMRI chomatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211			7.56	3.5E-01 X64585.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12014	24313			2.03	3.5E-01 AE001774.1	NT	Thermotoga maritime section 86 of 136 of the complete genome
12209	24433			2.21	3.5E-01 AE001691.1	NT	Thermotoga maritime section 3 of 136 of the complete genome
12843	24850	30625		2.64	3.5E-01 H80814.1	EST_HUMAN	ye54f1171 Soenes retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5
12843	24850	30626		2.84	3.5E-01 H80814.1	EST_HUMAN	ye54f1171 Soenes retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5
728	13359			1.5	3.4E-01 AJ242568.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13621	26136		7.62	3.4E-01 Y09798.2	NT	Pseudomonas fluorescens colR, cos genes, crf222 and partial fnaA gene
1013	13623	26138		8.97	3.4E-01 AW380120.1	EST_HUMAN	QV3-HT0281-241199-019-g10 HT0281 Homo sapiens cDNA
1371	13865	28481		1.86	3.4E-01 Y00554.1	NT	Anopheles stephensi rRNA gene for rRNA protein (positive regulatory element)
2445	15012	27294		2.6	3.4E-01 D80909.1	NT	Synechocystis sp. PCe8803 complete genome, 11/27, 1311235-1430418
3032	15848	28126		0.73	3.4E-01 AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15848	28127		0.73	3.4E-01 AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3183	157983	28268		0.96	3.4E-01 D80908.1	NT	Synechocystis sp. PCe8803 complete genome, 11/27, 1311235-1430418
3197	15809	28282		6.78	3.4E-01 U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3387	15689	28473		0.84	3.4E-01 AF034982.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3684	16188	28671		4.84	3.4E-01 AF108835.1	NT	Methylyovulus sp. strain SS1 putative CtpE (grpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds
3688	16493			1.32	3.4E-01 BF449010.1	EST_HUMAN	7N94801.X1_NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:O8LU15
4108	16702			1.23	3.4E-01 AF184914.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4123	16718			1.96	3.4E-01 AA584186.1	EST_HUMAN	nt!1b10.s1 NC1 CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4594	17177	28624		0.7	3.4E-01 AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4748	17330	29773		2	3.4E-01 BE068912.1	EST_HUMAN	MR4-BT0403-230200-202-001 BT0403 Homo sapiens cDNA
4785	17348	29785		1.01	3.4E-01 BF314689.1	EST_HUMAN	601801632F1 NIH MG3C_19 Homo sapiens cDNA clone IMAGE:4130635 5'
5087	17880			4.2	3.4E-01 A1240673.1	EST_HUMAN	q85c05.x1 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1887208 3' similar to contains Alu repetitive element
5384	18498	31210		2.8	3.4E-01 AL161584.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
53979	18559			5.68	3.4E-01 AA085313.1	EST_HUMAN	zn12d11.s1 Stratego 11NT neuron (#837233) Homo sapiens cDNA clone IMAGE:5477221 3'
6158	18771			2.44	3.4E-01 L02971.1	NT	Echivina 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181 18791	31560	0.69	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MCG_55 Homo sapiens cDNA clone IMAGE:38338926 3'	
6258 18865	31635	2.45	3.4E-01	AW204505.1	EST_HUMAN	U1+H-B11- 12-0-U .s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27188923	
6382 18898	31766	1.62	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hAmy2) Homo sapiens cDNA clone IMAGE:24495	
6841 19431		1.32	3.4E-01	N85225.1	EST_HUMAN	zb53e12.11 Scares_fetal_lung_NbHL16W Homo sapiens cDNA clone IMAGE:307342 3'	
7027 19561	32389	1.09	3.4E-01	AI468982.1	EST_HUMAN	Im63g05.11 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2102840 3' similar to gb:S37431	
7847 20389		0.51	3.4E-01	AE000493.1	NT	LAMININ RECEPTOR (HUMAN)	
8179 20720	33635	0.51	3.4E-01	Y14820.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome	
8424 20864		1.82	3.4E-01	AA337083.1	EST_HUMAN	Homo sapiens TRCAV28 gene, allele A4, partial	
8498 21037	33958	0.88	3.4E-01	LD46890.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome	
8788 21325	34249	1.63	3.4E-01	96333624	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds	
9139 21674	34616	3.89	3.4E-01	P28013	SWISSPROT	Batrachosarvus strauchi K2577, complete genome	
9139 21674	34617	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR	
9342 21858		0.59	3.4E-01	AB017610.1	NT	Ephydium fluviatile mRNA for PLC-gammaS, complete cds	
9357 20308	33208	4.77	3.4E-01	U18482.1	NT	Saccharomyces cerevisiae Mar1p (MAF1) gene, complete cds	
9357 20308	33209	4.77	3.4E-01	U18482.1	NT	Saccharomyces cerevisiae Mar1p (MAF1) gene, complete cds	
9612 22112	35075	0.88	3.4E-01	U88763.1	NT	Glycine max putative transcription factor SCOF-1 (scad-1) mRNA, complete cds	
9804 22302	35288	1.89	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18	
10373 22867		0.54	3.4E-01	AE004098.1	NT	Vibrio cholerae chromosome 1, section 4 of 251 of the complete chromosome	
10895 23416		4.42	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 101844 to 1029212 (section 87 of 148) of the complete genome	
10932 23450	36471	2.61	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN.	
10968 23484	36512	2.72	3.4E-01	AF045881.1	NT	Rutulus arcasi cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	
11184 23807	38718	1.89	3.4E-01	M25850.1	NT	Human von Willebrand factor gene, exons 36 and 37	
11184 23871	38717	1.89	3.4E-01	M25850.1	NT	Human von Willebrand factor gene, exons 38 and 37	
11372 23824	38887	2.27	3.4E-01	AB036607.1	NT	Rattus norvegicus mRNA for α -globin/MUC18, complete cds	
11401 23852	38917	4.38	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	
11614 24056	37121	1.75	3.4E-01	BF061948.1	EST_HUMAN	7168d12.21 NCI CG8 Homo sapiens cDNA clone IMAGE:3480843 3'	
11655 24082		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds	
11771 24160		1.44	3.4E-01	Z21621.1	NT	Saccharomyces RIB5 gene encoding Riboflavin synthase	
11873 24836		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds	
11998 24203		14.59	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24885			3.18	3.4E-01 BE218852.1	EST_HUMAN	Iw42h08_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTTR5_3
12079	24974			2.44	3.4E-01 98338361	NT	PTTR5 repetitive element: Beta vulgaris mitochondrial, complete genome
12198	24424	30850		2.66	3.4E-01 A1287131.1	NT	Mus musculus SII_MAP_17, CYP_4, SCL & CYP_b genes
12427	25068			1.25	3.4E-01 AJ2886948.1	NT	Claesdrium cellulolyticum partial spcVIB gene and spcVA gene, strain ATCC 35319
12623	24639			2.66	3.4E-01 AF019413.1	NT	Homo sapiens HLA class III region containing tenascin-X gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hofcasse (SK12W), RD, complement factor B (B), and complement component C2 (C2) genes,>
12851	24723			2.71	3.4E-01 11406174	NT	Neoglycera gruberi mitochondrion, complete genome
16	12685	25151		13.68	3.3E-01 X07880.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1J nadX gene
110	12895	26161		3.75	3.3E-01 X07880.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1J nadX gene
473	13108	25589		1.08	3.3E-01 AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
661	13285	25798		1.87	3.3E-01 7882485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1242	13840	28353		2.88	3.3E-01 Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1350	13945	28469		3.58	3.3E-01 BF588890.1	EST_HUMAN	60218401611 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:450025_3'
1649	14241	28775		1.43	3.3E-01 6753885	NT	Mus musculus disintegrin 5 (Digr5), mRNA
1773	14363			1.44	3.3E-01 AA332734.1	EST_HUMAN	EST367222 Embryo, 8 week Homo sapiens cDNA 5' end
2075	14655			1.22	3.3E-01 AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2450	15017			5.41	3.3E-01 4507834	NT	(Homo sapiens uridine monophosphate synthetase (uridate phosphoryl transferase) and orotidine-5'-decarboxylase) (UMPS) mRNA
2976	15592	28074		2.14	3.3E-01 AJ251805.1	NT	Bacteriophage phi-YG03-12 complete genome
3049	15685			0.65	3.3E-01 002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12a) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF_P35)
3091	15708	28178		0.82	3.3E-01 AJ007832.2	NT	Streptomyces arigacca mithramycin biosynthetic genes
3542	16147	28659		0.89	3.3E-01 AB012922.1	NT	Homo sapiens MTA-L1 gene, complete cds
3882	16490	28942		2.14	3.3E-01 OB84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3890	16489	28949		0.85	3.3E-01 P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4037	16635	29104		1.49	3.3E-01 AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4073	16689	29130		1.95	3.3E-01 AF200448.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4457	17043			1.44	3.3E-01 D31662.1	NT	Reitius moneugicus DNA for regucalcin, partial cds
4789	17377			1.57	3.3E-01 AL530114.1	EST_HUMAN	tp78b12_x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:22056407 3' similar to gb:J57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN)
4984	17538	28890		1.44	3.3E-01 DB4003.1	NT	Synechocystis sp. PCG6803 complete genome, 22/27, 2755703-2888766

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18159	30573	2.75	3.3E-01	X88818.1	NT	R. <i>norvegicus</i> mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X88818.1	NT	R. <i>norvegicus</i> mRNA for 3'UTR of ubiquitin-like protein
6101	18717	31468	1.72	3.3E-01	BE6108650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18717	31469	1.72	3.3E-01	BE6108650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6188	18789	31507	12.71	3.3E-01	P05691	SWISSPROT	CIRCUIMSPOROZOITE PROTEIN (CS)
6969	19546	32359	4.8	3.3E-01	A1628131.1	EST_HUMAN	P84401.1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:22655809 3' similar to contains Ala repetitive element;contains element L1 repetitive element;
6969	19546	32370	4.8	3.3E-01	A1628131.1	EST_HUMAN	P84401.1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:22655809 3' similar to contains Ala repetitive element;contains element L1 repetitive element;
7758	20266	33182	1.81	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone IMAGE:4301800 5'
8497	21036	33957	17.55	3.3E-01	BF883384.1	EST_HUMAN	60214037ZF1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8683	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8688	21235	34157	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8688	21235	34158	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9042	21579	34508	0.83	3.3E-01	Q82925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAP/ERK KINASE KINASE 1) MEK KINASE 1 (MEKK 1)
9300	21800	34848	0.89	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9300	21800	34849	0.89	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9430	21839	34887	3.24	3.3E-01	N68898.1	EST_HUMAN	2267101.11 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287849 3'
9471	21870	34819	2.83	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-904 TN0077 Homo sapiens cDNA
9802	22389	2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds	
10600	23134	36147	2.83	3.3E-01	X638953.1	NT	D.mauritiana Adh gene
10600	23134	36148	2.83	3.3E-01	X638953.1	NT	D.mauritiana Adh gene
10805	23424	1.8	3.3E-01	BF528448.1	EST_HUMAN	602070802F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213585 5'	
11110	23620	36861	17.52	3.3E-01	BE2198351.1	EST_HUMAN	h51022.1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176818 3'
11223	23754	36812	4.97	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11565	24012	4.68	3.3E-01	AA806821.1	EST_HUMAN	ab7102.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone pFL5J1 nodX gene	
11584	12885	25151	2.48	3.3E-01	X07890.1	NT	Rhizobium leguminosarum symb plasmid pFL5J1 nodX gene
11759	24153	36771	1.98	3.3E-01	6568319	NT	Homo sapiens adenylyl adenosine 1 (AOX1), mRNA
12510	24631		36.28	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
482	13115		1.78	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Episin mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13387			0.76	3.2E-01 AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13804	28317		27.98	3.2E-01 AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA polymerase gene, complete cds
1325	13919	28441		1.39	3.2E-01 Z50202.1	NT	<i>P. vulgaris</i> arc5-1 gene
1434	14027	28555		7.37	3.2E-01 Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	28946		0.92	3.2E-01 Z38041.1	NT	<i>S. cerevisiae</i> chromosome II reading frame ORF YBR1172c
1819	14409	28954		6.36	3.2E-01 AW657194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1819	14409	28955		6.36	3.2E-01 AW657194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1883	14469	27028		1.22	3.2E-01 AL111655.1	NT	Babrytae chinensis strain T4 cDNA library under conditions of nitrogen deprivation
2205	14781	27354		2.89	3.2E-01 BF203817.1	EST_HUMAN	6011883804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:41115125'
2578	15140			2.24	3.2E-01 7710079 NT	NT	Mus musculus Pbx/Knotched 1 homeobox (Pbxnuc1), mRNA
2734	15289	27857		1.09	3.2E-01 AF080568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3668	16269			0.78	3.2E-01 D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16821			0.61	3.2E-01 AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4483	17088	28518		1.64	3.2E-01 M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	28828		1.58	3.2E-01 Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17322			6.52	3.2E-01 BF863817.1	EST_HUMAN	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P99)
5009	17582	30025		0.63	3.2E-01 Q57081	SWISSPROT	EST_HUMAN
5174	17741	30170		0.58	3.2E-01 BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38887995
5392	17850	30363		0.83	3.2E-01 AY08847.1	NT	Homino sapiens Interleukin 12 p40 subunit (IL12B-1 allele, complete cds
5476	18110	30519		2.5	3.2E-01 BE179584.1	EST_HUMAN	CHD-HT1568-060300-268-f10 HTT0568-Homo sapiens cDNA
61112	18728	31481		1.18	3.2E-01 L27221.1	NT	Giardia intestinalis pyruvate flavodoxin oxidoreductase and flanking genes
68331	18421			1.03	3.2E-01 AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAAC0361 protein
8113	20054	33563		1.33	3.2E-01 M60286.1	NT	Rat ISO-2alpha neuropeptide factor gene, complete cds
8210	20751	33665		0.51	3.2E-01 AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12W/ox1
8308	20849	33772		1.34	3.2E-01 X02508.1	NT	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777		16.78	3.2E-01 BF311635.1	EST_HUMAN	6011897707F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:41268335'
8338	20838			1.43	3.2E-01 AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20877	33891		1.22	3.2E-01 BF248771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:40756275
8437	20877	33892		1.22	3.2E-01 BF248771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:40756275
8508	21047	33968		2.72	3.2E-01 AE002015.1	NT	Deinococcus radiodurans R1 section 152 of the complete chromosome 1
8605	21144	34058		0.69	3.2E-01 U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-e2) gene, partial cds

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88605	21144	34059	0.68	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-e2) gene, partial cds
88897	21535	34485	0.58	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
89007	21544		2.08	3.2E-01	M88511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21613	34547	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 8-phosphofructose-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21613	34548	0.48	3.2E-01	AF041829.1	NT	Homo sapiens 8-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
98905	22402	35376	3.22	3.2E-01	U44914.1	NT	Barrelle budorferi plasmid cp32-2, cpC and cpD genes, complete cds, and unknown genes
10100	22595	35588	0.51	3.2E-01	BE326230.1	EST_HUMAN	h68905.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568-3'
10213	22703		3.03	3.2E-01	ABD1138.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36098	3.28	3.2E-01	T05813.1	EST_HUMAN	EST047022 Fetal brain, Stratagene (cat#8362026) Homo sapiens cDNA clone HFBDZ21
11786	24989		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12344	24525		4.85	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12441	24819		3.37	3.2E-01	AF157625.1	NT	Bos taurus intestinal 1,4,5-triphosphate receptor type 1 mRNA, complete cds
12489	24818		1.94	3.2E-01	L36874.1	NT	Homo sapiens deoxyribonuclease deaminase gene, complete cds
12550	25041	30504	1.98	3.2E-01	BE385778.1	EST_HUMAN	601275480F1 NIH_MCGC_20 Homo sapiens cDNA clone IMAGE:3618748-5'
26985	15252	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	ye60108.71 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051-5 similar to gb:MG4241 OM PROTEIN (HUMAN);
27722	15403	27843	3.67	3.1E-01			Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
27722	15403	27844	3.67	3.1E-01			Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2885	15501		1.35	3.1E-01	AW629308.1	EST_HUMAN	h46808.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391-3'
32093	15820		3.53	3.1E-01	ABD29068.1	NT	Mus musculus gene for Sart/Thr kinase KKI/AMRE, exon 6
39778	16578	29046	0.91	3.1E-01	AJ251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
50555	17628	30072	0.78	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rat], Sprague-Dawley, lung, mRNA, 1205 nt]
5097	17670	30108	0.82	3.1E-01	AE03384.1	NT	Xylella fastidiosa, section 130 of 228 of the complete genome
52098	17771	30184	0.98	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
56689	18298	30778	10.8	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5788	18411	31127	0.75	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141W
5798	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polyysin
5945	18585	31285	2.18	3.1E-01	AF164122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
65592	19189	31892	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-004 HN0001 Homo sapiens cDNA
68554	18250	32052	0.87	3.1E-01	AI284458.1	EST_HUMAN	q138001.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874689-3'
6784	18375	32191	0.81	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
68683	18597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281089-005-H05 CT0222 Homo sapiens cDNA

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7048	24741	30458	2.4	3.1E-01	BE7377392.1	EST_HUMAN	6013061121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7671	20183	33071	1.18	3.1E-01	4885380 NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA	
85582	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	yg46011.81 Scores: infant brain TNIB Homo sapiens cDNA clone IMAGE:36639 3'
8818	22314	35295	0.45	3.1E-01	68769322 NT	Mus musculus phosphatidylinositol-4-phosphate 5'-kinase, type 1 gamma (PIP5K1G), mRNA	
8978	22474	35458	0.81	3.1E-01	BF886639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
8978	22474	35457	0.81	3.1E-01	BF886639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10035	22530	35525	1.7	3.1E-01	AI244001.1	EST_HUMAN	q81611X1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1883980 3' similar to gb:S65700 HYDROXYMETHYL GLUTARYL-COA LYASE PRECURSOR (HUMAN)
10204	22689		0.54	3.1E-01	T55325.1	EST_HUMAN	gb:4708.81 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74367 3' similar to gb:MA1038_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	36261	1.96	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096814 5'
11411	23882	36923	2.03	3.1E-01	7062281 NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA	
11821	24257		2.13	3.1E-01	AF284308.1	NT	Andis opalinus isolate Q5 NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11880	24282		1.85	3.1E-01	AF304162.1	NT	Stizoidion vitreum 40S ribosomal protein S11 mRNA, partial cds
12108	24370		3.31	3.1E-01	AF195853.1	NT	Homo sapiens membrane-bound antipeptidase P (XNPEP2) gene, complete cds
12498	24624		3.89	3.1E-01	AF196778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JMS protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel &
12535	25035		1.62	3.1E-01	109466923 NT	NT	Mus musculus peptidoglycan recognition protein-like (Pgrlp)-pending, mRNA
78	15382	25224	1.37	3.0E-01	6755083 NT	NT	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
275	12832	25419	11.51	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1268	13883	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	zsc3f08.21 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1555	14147	26880	6.84	3.0E-01	AJ008755.1	NT	Bleemopatra physalus gene encoding atrial natriuretic peptide
3248	15860		1.4	3.0E-01	AB033481.1	NT	Corynebacterium sp. ALY-1 alpPG gene for polyglutonate lyase, complete cds
38932	16530	28887	2.1	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281198-001-001 ST0262 Homo sapiens cDNA
4048	16843	29109	1.01	3.0E-01	AJ2271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4611	17194	29840	1.78	3.0E-01	AJ008755.1	NT	Bleemopatra physalus gene encoding atrial natriuretic peptide
55534	18186	30561	5.34	3.0E-01	BE741628.1	EST_HUMAN	601594980F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5627	18256	30726	0.88	3.0E-01	AF229247.1	NT	Centraglobi orthopoxvirus hemagglutinin gene, complete cds
56895	18321	30820	4.03	3.0E-01	BE893575.1	EST_HUMAN	RC3-BT0333-180700-111-003 BT0333 Homo sapiens cDNA
56895	18321	30821	4.03	3.0E-01	BE893575.1	EST_HUMAN	RC3-BT0333-180700-111-003 BT0333 Homo sapiens cDNA
5731	18357	31062	4.57	3.0E-01	U01247.1	NT	Mus musculus 129svClara cell 10 kd protein (mCC10) gene, complete cds
6919	18578	32407	3.14	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944 18052	30475	0.7	3.0E-01	U02369.1	NT	Stronglyacentrinous purpuratus 34 kDa laminin-binding protein mRNA, partial cds	
7005 19503	32322	0.98	3.0E-01	AF228247.1	NT	Cantigalo orthopoxvirus hemagglutinin gene, complete cds	
7175 19707	32555	0.78	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006	
7387 19893	32758	6	3.0E-01	10847007 NT	Mus musculus midolloin (Midin-pending), mRNA		
7512 20033	32899	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds	
7887 20409	33316	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome	
8314 20855			3.82	3.0E-01	8910161 NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clectf9), mRNA	
8411 20951	33870	1.27	3.0E-01	BE5680083.1	EST_HUMAN	G011339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881594 5'	
8783 21302	34223	0.82	3.0E-01	AF141678.1	NT	Streptomyces sulfurofaciens isopenicillin N synthase (pcdC) gene, partial cds	
8805 21344		0.95	3.0E-01	78816885 NT	Homo sapiens DKFZP588M0122, protein (DKFZP588M0122), mRNA		
9145 21680	34824	0.98	3.0E-01	AF220507.1	NT	Anabaena PCG7120 cytosine-specific DNA methyltransferase (dnmB) gene, complete cds; putative arabinose phosphotobioisomerase gene, partial cds; and unknown gene	
9493 21683	34949	0.65	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 kD PROTEIN IN WZA/ASMA INTERGENIC REGION	
9878 22375	35352	0.84	3.0E-01	BF574612.1	EST_HUMAN	G02133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'	
10294 22788	35778	0.58	3.0E-01	AW118111.1	EST_HUMAN	x03410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'	
10298 22780	35780	1.95	3.0E-01	AB030231.1	NT	Aspergillus oryzae btpA gene for ER chaperone BiP, complete cds	
10315 22809	35801	0.73	3.0E-01	BF883841.1	EST_HUMAN	G02140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'	
10315 22809	35802	0.73	3.0E-01	BF883841.1	EST_HUMAN	G02140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'	
11604 24047	37112	2.87	3.0E-01	HE10281	EST_HUMAN	yp84610.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:104107 5'	
11604 24047	37113	2.87	3.0E-01	H51028.1	EST_HUMAN	yp84610.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:104107 5'	
11975 24267		1.37	3.0E-01	PS44880	SWISSPROT	PONTICULIN PRECURSOR	
12227 24984	2893	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glycanaldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)		
12528 25033		2.51	3.0E-01	8677768 NT	Mus musculus fibose 5'-phosphatase isomerase A (Rplp), mRNA		
1824 14509	27084	2.27	2.9E-01	5174502 NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA		
2070 14650	27221	1.38	2.9E-01	AE0009736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome	
2524 15088		1.22	2.9E-01	M32280.1	NT	Mouse adipoprotein A-1 (Ab-2) gene, complete cds	
3289 15900	28379	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-412 CT0328 Homo sapiens cDNA	
3289 15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-412 CT0328 Homo sapiens cDNA	
3885 16563	28032	0.71	2.9E-01	AI610683.1	EST_HUMAN	f21le11.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A Zinc FINGER PROTEIN (HUMAN);contains element L1 repetitive element;	
4159 16751		0.67	2.9E-01	AW002902.1	EST_HUMAN	W02F10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'	
4583 17168	29609	1.21	2.9E-01	AA284468.1	EST_HUMAN	z557d12.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701581 5' similar to contains Alu repetitive element;	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4783	17372		0.63	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5148	17718		1.02	2.9E-01	U80756.1	NT	Lymantria dispar vitelliferin gene, complete cds
5154	17724	30155	1.43	2.9E-01	7682190	NT	Homo sapiens KIAA0537 gene product (KIAA0537), mRNA
5285	17847		1.7	2.8E-01	AI870899.1	EST_HUMAN	we0803_x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element;
5463	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	Y77612_x1 Soesres infant brain Nb24Pb homo sapiens cDNA clone IMAGE:28291 3'
5582	19522	32344	0.79	2.8E-01	AF321001.1	NT	Suedea maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5837	18558	31288	5.1	2.8E-01	X56098.1	NT	B. subtilis levansucrase operon levO, levE, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansucrase
5837	18558	31287	5.1	2.8E-01	X56098.1	NT	B. subtilis levansucrase operon levO, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansucrase
5949	18570	31302	6.03	2.8E-01	6679882	NT	Mus musculus Eph receptor AB (Ephab6), mRNA
6208	18816	31587	1.28	2.9E-01	AA418145.1	EST_HUMAN	Z697b12_x1 Soesres NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6427	19030	31813	0.83	2.8E-01	AI787128.1	EST_HUMAN	we27G05_x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element;
6467	19068	31854	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6585	19163	31983	0.72	2.9E-01	R68194.1	EST_HUMAN	Y39d08_x1 Soesres placenta Nb24Pb Homo sapiens cDNA clone IMAGE:111615 5'
6585	19163	31984	0.72	2.9E-01	R68194.1	EST_HUMAN	Y39d08_x1 Soesres placenta Nb24Pb Homo sapiens cDNA clone IMAGE:111615 5'
7062	18081	30437	1.35	2.9E-01	AF142328.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7153	19885	32527	2.87	2.9E-01	Q04298	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7213	19744	32598	1.81	2.9E-01	AF100958.1	NT	Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapash (tapash), Raf/GDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl) transferase, complete cds
7860	20402	33308	1.82	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33308	1.92	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20844		0.88	2.9E-01	BF217743.1	EST_HUMAN	601862570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	33900	0.68	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8856	21395	34318	1.07	2.9E-01	AF225308.1	NT	Arabidopsis thaliana sulfonurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34688	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 546
9170	21747	34690	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 546
10773	23287	36302	2.24	2.9E-01	AF28843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23555	38598	2.88	2.9E-01	VO1394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23555	36590	2.88	2.9E-01	VO1394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	36870	2.07	2.8E-01	AA835373.1	EST_HUMAN	ny35h02.61 NCI_CGAP_Pt12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8
11456	23906	36873	5.52	2.8E-01	AL138078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5'6 wZB8R05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2585921 3' similar to contains element MER29 repetitive element;
12172	24411	30944	1.64	2.8E-01	AW005871.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12262	24472	30932	1.47	2.8E-01	AF082453.1	NT	601482059F1 NIH_MGC_68 Homo sapiens cDNA clones IMAGE:3884659 5'
12313	24505		1.4	2.8E-01	BE788189.1	EST_HUMAN	Chlamydomyces reinhardtii mRNA 1 for nitrite reductase structural locus
12588	24879	30877	1.57	2.8E-01	Y08937.1	NT	Chlamydomyces reinhardtii mRNA 1 for nitrite reductase structural locus
12588	24879	30878	1.57	2.8E-01	Y08937.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
594	13224		2.08	2.8E-01	U87738.1	NT	Prunus dwarf virus movement protein, complete cds; coat protein, complete cds
599	13228		0.75	2.8E-01	L28145.1	NT	Guita guina oocyte maturation factor Moa (c-mos) gene, partial cds
1122	13725	28238	3.14	2.8E-01	AF168050.1	NT	QV1-C70384-12/2000-065 CTU384 Homo sapiens cDNA clone IMAGE:3163888 5'
1320	13814	28435	3.51	2.8E-01	BE313442.1	EST_HUMAN	60148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1320	13914	28436	3.51	2.8E-01	BE313442.1	EST_HUMAN	60148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1334	13928	28446	1.03	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1785	14355	28902	2.01	2.8E-01	AW890020.1	EST_HUMAN	QV1-C70384-12/2000-065 CTU384 Homo sapiens cDNA DKFZp586I2321
2057	14638	27710	2.12	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586I2321 r1 588 (synonym: huts1) Homo sapiens cDNA clone IMAGE:2912333 3'
2175	14752	27322	3.53	2.8E-01	AW511195.1	EST_HUMAN	hd44503.x1 Soorees_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:3163888 5'
25111	15073	27848	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
25111	15075	27849	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2584	16147		2.76	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
26988	15246	27813	1.21	2.8E-01	AB022875.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
28988	15614		1.7	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
28989	16816	28094	2.38	2.8E-01	Z14037.1	NT	B. tauris microsatellite (ETH121)
28989	15615	28095	2.38	2.8E-01	Z14037.1	NT	B. tauris microsatellite (ETH121)
3425	16033	28513	1.28	2.8E-01	AP00004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-884000 nt, position (4/7)
4068	16884	28126	2.08	2.8E-01	AE001180.1	NT	Bornetia burgdoferi (section 68 of 70) of the complete genome
4202	16791		0.62	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4276	16882		2.75	2.8E-01	AJ080888.1	EST_HUMAN	6044910J1 Soorees_betais_NHT Homo sapiens cDNA clone IMAGE:1640283 similar to contains AU repetitive element/contains element MER22 repetitive element;
4553	-17136	28584	1.32	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Mage8 gene, Calretinin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4559	17142	28589	2.47	2.8E-01	P13815	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN)(L PROTEIN)
4697	17472	28928	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	28929	1.07	2.8E-01	D15050_1	NT	Human mRNA for transcription factor AREB8, complete cds
4837	17512	28958	1.02	2.8E-01	AW584539_1	EST_HUMAN	hg38d05_x1 NCI CGAP Gc8 Homo sapiens cDNA clone IMAGE:2850568 3'
4949	17524	28985	1.17	2.8E-01	AF073238_1	NT	Hepatitis G Virus Isolate 60 (S2NAE12) polyprotein precursor, gene, partial cds
4955	17530	28972	3.5	2.8E-01	AF030154_1	NT	Bovine adenovirus 3 complete genome
4986	17560	30003	1.67	2.8E-01	BF528188_1	EST_HUMAN	602042601F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4180128 5'
5013	17587	30030	2.82	2.8E-01	AI272689_1	EST_HUMAN	qf8C11.1x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1870628 3' similar to contains Au repetitive element; contains element LTR5 repetitive element;
6514	24744	30568	21.59	2.8E-01	AA34997_1	EST_HUMAN	EST167072 Infant brain Homo sapiens cDNA 5' end
5781	18416	31132	2.78	2.8E-01	AB016225_1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.87	2.8E-01	AW882583_1	EST_HUMAN	CMT-BN0024-150200-118-912 BN0024 Homo sapiens cDNA
6078	18895	31442	0.68	2.8E-01	AA785288_1	EST_HUMAN	c01606_51 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303891 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);
6323	25114		0.75	2.8E-01	M36688_1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6368	18970	31748	1.55	2.8E-01	AF003124_1	NT	Mesembryanthemum crystallinum fructose-biphosphate esterase mRNA, complete cds
6366	18970	31749	1.55	2.8E-01	AF003124_1	NT	Mesembryanthemum crystallinum fructose-biphosphate esterase mRNA, complete cds
6829	19419	32225	8.4	2.8E-01	BF511215_1	EST_HUMAN	UH-B14-ach-4-04-0-U1.51 NCI CGAP_Sub9 Homo sapiens cDNA clone IMAGE:3085182 3'
7467	19889		1.19	2.8E-01	U05633_1	NT	Marsilea quadrifolia ribulose-1,5-biphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20278	33174	0.68	2.8E-01	BE537151_1	EST_HUMAN	6010631035F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449568 5'
8036	20578	33432	1.12	2.8E-01	AI346128_1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); cp48h01_x1 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1826289 3' similar to gb:J06323_cds1
8038	20578	33433	1.12	2.8E-01	AI346128_1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20691	33605	2.18	2.8E-01	U51688_1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8451	20991	33909	0.47	2.8E-01	AA911629_1	EST_HUMAN	af02h05_51 NCI CGAP_Co12 Homo sapiens cDNA clone IMAGE:1418883 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8525	21064		6.69	2.8E-01	BF347847_1	EST_HUMAN	602022887F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158525 5'
8387	21810	34761	1.22	2.8E-01	U17251_1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
9627	22127		1.03	2.8E-01	L13654_1	NT	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
9803	22301	35286	1.04	2.8E-01	AF132728_1	NT	Escherichia coli translocated intimin receptor Tr (tr) gene, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728_1	NT	Escherichia coli translocated intimin receptor Tr (tr) gene, complete cds
9881	22358	35398	0.84	2.8E-01	AF294383_1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9972	22467	35451	1.91	2.8E-01	7708163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA

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Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
102115	22710		0.81	2.8E-01	9828154	NT	Fujinami sarcoma virus, complete genome
102555	22750	35738	0.47	2.8E-01	BE959727.2	EST_HUMAN	601654622R1 NIH_MG3C_57 Homo sapiens cDNA clone IMAGE:3839785 3'
106222	23154	36168	2.26	2.8E-01	BF241082.1	EST_HUMAN	601880784F1 NIH_MG3C_56 Homo sapiens cDNA clone IMAGE:4106350 5'
106222	23154	36167	2.28	2.8E-01	BF241082.1	EST_HUMAN	601880784F1 NIH_MG3C_56 Homo sapiens cDNA clone IMAGE:4106350 5'
106511	23183	36197	2.83	2.8E-01	BF865870.1	EST_HUMAN	601852148F1 NIH_MG3C_58 Homo sapiens cDNA clone IMAGE:4078028 5'
10760	23284	36297	3.31	2.8E-01	AF051682.1	NT	Drosophila heteroneura fruless (mu) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11158	23685		4.56	2.8E-01	BF874023.1	EST_HUMAN	602137418F1 NIH_MG3C_83 Homo sapiens cDNA clone IMAGE:4273853 5'
122113	24436		15.74	2.8E-01	D83328.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178899.1	EST_HUMAN	PM4-H10608-030400-001-a07 HT0808 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE800116.1	EST_HUMAN	601673020F1 NIH_MG3C_21 Homo sapiens cDNA clone IMAGE:38555896 5'
12519	24988		2.21	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DNPK-IIK2) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17322.1	NT	Rattus norvegicus CDK104 mRNA
641	13264	25740	2.53	2.7E-01	AA450061.1	EST_HUMAN	z239610.s1 Scabies_low_fetus_Nb24-ff8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1304	13888	28418	1.89	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tp100 gene for transposases, complete cds
1882	14255		2.17	2.7E-01	X78815.1	NT	Gambelia SB2 gene
1787	14357	28903	3.34	2.7E-01	W58087.1	EST_HUMAN	z22210.71 Scabies_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	28948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].
2181	15459		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular membrane transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITTOQ88PfU (M88), partial
2486	15080	27634	3.82	2.7E-01	AI310858.1	EST_HUMAN	ta3c1132 NCI_CGA_P_LU25 Homo sapiens cDNA clone IMAGE:2046833 3' similar to contains element L1 repetitive element;
3013	15629		0.73	2.7E-01	BF0886284.1	EST_HUMAN	CM1-H106075-060600-385-a05 HT08075 Homo sapiens cDNA
4082	16678	29138	1.88	2.7E-01	AI928015.1	EST_HUMAN	w02511.X1 NCI_CGA_P_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4098	16691	29147	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 8 (eE8) gene, partial cds
4096	16691	29148	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 8 (eE8) gene, partial cds
4101	16695	29151	2.31	2.7E-01	L77580.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
6020	17594	30037	0.98	2.7E-01	L27616.1	NT	Triticum aestivum (Wcs88) gene, complete cds
5183	17758		3.82	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0288-230/200-016-a03 CT0288 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	P17277	SWISSPROT	HOMEobox PROTEIN HOXA4 (CHOX-1.4)
6681	18398		0.88	2.7E-01	AB063317.1	NT	Astrocapsa myrophitolina mitochondrial Cytb gene for cytochrome b, partial cds
6724	18318	32122	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	188118	32123	1.07	2.7E-01 AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome	
6875	188099	32443	2.03	2.7E-01 Q61594	SWISSPROT	FIBRILLIN 1 PRECURSOR	
						Drosophila melanogaster rfc-40 protein, Rap protein (Rop), and small GTP binding protein (DRLs-2) genes, complete cds	
7085	188558	32495	0.76	2.7E-01 U15987.1	NT		
7393	188118	32782	0.87	2.7E-01 Q111079	SWISSPROT	HYPOTHETICAL 20 kD PROTEIN B05683.3 IN CHROMOSOME X	
7582	20079	32854	0.95	2.7E-01 Q011688	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1	
7582	20079	32855	0.95	2.7E-01 Q011688	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1	
7677	20188	33078	2.21	2.7E-01 AF248054.1	NT	Bos taurus microtuber calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	
7677	20188	33077	2.21	2.7E-01 AF248054.1	NT		
7720	20228	33118	0.82	2.7E-01 AA351121.1	EST HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H	
7720	20228	33117	0.92	2.7E-01 AA351121.1	EST HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H	
7805	20348	33258	0.95	2.7E-01 AA013147.1	EST HUMAN	2835011.81 Soares retina N264HR Homo sapiens cDNA clone IMAGE:3803657 3' similar to contains AU repetitive element	
7869	20511		0.51	2.7E-01 AF048820.1	NT	Catassus auratus pituitary adenylyl cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds	
8078	208221	33534	0.58	2.7E-01 AW886503.1	EST HUMAN	MR1-SN00862-100500-002-008 SN00862 Homo sapiens cDNA	
8127	208688	33577	0.48	2.7E-01 R39257.1	EST HUMAN	ycg1h06.51 Soares Infant brain 1NIH Homo sapiens cDNA clone IMAGE:235113	
82322	20773	33694	0.94	2.7E-01 AL161552.2	NT	Arribalzaga thalama DNA chromosome 4, contig fragment No. 52	
8864	21233	34154	0.83	2.7E-01 Q14784	SWISSPROT	MAJOR VALL PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)	
8897	21495	34410	0.53	2.7E-01 X03216.1	NT	Staphylococcus aureus transposon Tn554	
9258	21782	34734	0.83	2.7E-01 Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THERRS)	
9258	21782	34735	0.83	2.7E-01 Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THERRS)	
9259	21785		2.02	2.7E-01 P37928	SWISSPROT	FIMBRIAE W PROTEIN	
9716	22214	35189	0.67	2.7E-01 D86660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds	
9963	22498	35476	0.91	2.7E-01 AF091848.1	NT	Oncotique curculio calgranulin C mRNA, partial cds	
10028	22521		2.5	2.7E-01 AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds	
10148	22843	35634	0.69	2.7E-01 AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9	
10148	22843	35635	0.69	2.7E-01 AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9	
10691	23221	36233	2.31	2.7E-01 AV705043.1	EST HUMAN	AV705043 ADB Homo sapiens cDNA clone ADIBC0D05 5'	
10691	23221	36234	2.31	2.7E-01 AV705043.1	EST HUMAN	AV705043 ADB Homo sapiens cDNA clone ADIBC0D05 5'	

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	36244	3.65	2.7E-01	AJ133289.1	NT	Homo sapiens cavinin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
122986	24863		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24627		3.86	2.7E-01	AF217491.1	NT	Homo sapiens fragile 1D caddo reductase (FOR) gene, exon 6
495	15416	25615	2.06	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
506	13139		1.24	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	28558	2.19	2.6E-01	BE885987.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1485	14078	28616	1.36	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 301K
1841	14525	27080	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1841	14525	27081	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
					bbo4d10.1x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M43072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactin surfactin 3 protein gene		
2140	14718		13.12	2.6E-01	AW733152.1	EST_HUMAN	(MOUSE);
2197	14773	27347	1.41	2.6E-01	M11844.1	NT	Human proelastin gene, complete cds
2512	15076		2.09	2.6E-01	Y12898.1	NT	B. maritimus rbcL gene
2583	15148		10.77	2.6E-01	BE272440.1	EST_HUMAN	601128016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:28900043 5'
3840	16243	28719	0.88	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3705	16808	28775	2.13	2.6E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4175	18798	29214	0.7	2.6E-01	AW865910.1	EST_HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4234	16822	29273	19.88	2.6E-01	BE080598.1	EST_HUMAN	QY1-BT0830-040400-132-003 BT0830 Homo sapiens cDNA
4448	17034	29477	1.57	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4593	17178	29822	0.78	2.6E-01	AB021180.1	NT	Genus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29823	0.76	2.6E-01	AB021180.1	NT	Genus gallus mRNA for skeletal myosin heavy chain, complete cds
4846	17228	29884	1.35	2.6E-01	AA457817.1	EST_HUMAN	seeded07_71 Strategene fetal retina B337202 Homo sapiens cDNA clone IMAGE:838477 5'
4752	17333	29776	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhc63*1) mRNA, complete cds
4825	17403	29856	1.47	2.6E-01	AF142703.1	NT	Ophrestis reticulosa matrice-like protein (mstK) gene, complete cds; chloroplast product yj51ad5.r1 Soares placentae Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
5107	17679	30118	3.58	2.6E-01	J04858.1	EST_HUMAN	am33b11.s1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488805 3'
5195	17760		0.98	2.6E-01	AA884625.1	EST_HUMAN	Paramecium caudatum gene for PAp, complete cds
5544	18178		1.29	2.6E-01	AB0235972.1	NT	
5840	18289	30742	0.88	2.6E-01	M80000.1	NT	Acetobacter xylinum cellulose synthase (bcaA) gene, partial cds, CMCAx and CepAx genes, complete cds

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5780	18388		0.81	2.8E-01	AJ882388.1	EST_HUMAN	Wt16a03_x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
5947	18388	31289	0.69	2.8E-01	AF207650.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pimr-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g?
6221	25113		2.38	2.8E-01	AE001811.1	NT	Thermobius maritima section 123 of 138 of the complete genome
6348	18653	31732	1.89	2.8E-01	AJ582557.1	EST_HUMAN	Is02a12_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 :contains element LTR1 repetitive element;
6348	18653	31733	1.89	2.8E-01	AJ582557.1	EST_HUMAN	Is02a12_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227439 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 :contains element LTR1 repetitive element;
6554	18152	31948	1.05	2.8E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 67
7103	18673	32512	0.97	2.8E-01	AB14980.1	EST_HUMAN	Wd48cd04_x1 Saccharomyces cerevisiae cDNA clone IMAGE:S1_Homo sapiens cDNA PRECURSOR (HUMAN); PEPTIDYL-GLYCINE-ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.98	2.8E-01	AL139077.2	NT	Campylobacter jejuni NCTC1118 complete genome; segment 4/8
7721	20220	33118	1.6	2.8E-01	R10385.1	EST_HUMAN	y31a03_s1 Saccharomyces cerevisiae cDNA clone IMAGE:128004 3' similar to gb:M37721
7781	20334	33240	1.14	2.8E-01	R02411.1	EST_HUMAN	gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7845	20387	33280	1.18	2.8E-01	BE144331.1	EST_HUMAN	Ye822a07_r1 Saccharomyces cerevisiae cDNA clone IMAGE:124212 S'
8083	20225	33538	0.67	2.8E-01	X82841.1	NT	MFD-H10160-181186-003-d12/H10160 Homo sapiens cDNA
8083	20225	33539	0.67	2.8E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1.2 mannosidase (Berlin)
8276	20817	33738	2.88	2.8E-01	BF343588.1	EST_HUMAN	602014422F1_NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:41190398 5'
8349	20890	33810	1.89	2.8E-01	Q10190	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8827	21168	34080	4.49	2.8E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8827	21168	34081	4.49	2.8E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8838	21811	34782	0.98	2.8E-01	X17804.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
8854	22153		0.5	2.8E-01	AF057121.1	NT	Larrea canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22290	35285	0.83	2.8E-01	P87388	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9782	22290	35288	0.83	2.8E-01	P87388	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10083	22988		0.5	2.8E-01	Q28285	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.81	2.8E-01	Y10198.1	NT	Homo sapiens PHEX gene
10500	22984		0.51	2.8E-01	AJ978891.1	EST_HUMAN	Wt58009_x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2491885 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11300	23752	36809	2.18	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.88	2.6E-01	X51755.1	NT	Human limboid-immunoglobulin constant region complex (germline)
11777	24165		1.72	2.6E-01	101906555	NT	Mus musculus Jerky (Jk), mRNA
11973	24691		4.08	2.6E-01	BE882491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912812' 5'
12042	24329	30998	4.8	2.6E-01	AF316896.1	NT	Homo sapiens NaK-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
12396	24558		1.34	2.6E-01	DBB425.1	NT	Canis cabeyae mRNA for serine/threonine kinase, complete cds
12478	24612		1.98	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
12526	24641		1.37	2.6E-01	AF141325.2	NT	Homo sapiens Inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12567	24698		3.74	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
262	12821	25407	1.48	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
263	12821	25407	1.77	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12833		4.28	2.5E-01	M28501.1	NT	Starfish (<i>P. ochraceus</i>) cytoplasmic actin gene, complete cds
885	13480	25994	1.02	2.5E-01	U08984.1	NT	<i>Mus musculus</i> ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.5E-01	AE002159.1	NT	Unpublished ureayticum section 57 of 59 of the complete genome
1160	13753	26274	11.59	2.5E-01	T88897.1	EST_HUMAN	ye11g07-11 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117488 5'
1568	14158	26889	0.87	2.5E-01	AL115824.1	NT	BoNT/Ms chinesa strain T4 cDNA library under conditions of nitrogen deprivation
1768	14356		6.08	2.5E-01	4885408	NT	<i>Mus musculus</i> hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1827	15454	27067	1.28	2.5E-01	BE886804.1	EST_HUMAN	PM4-C10400-310700-005-008 C10400 Homo sapiens cDNA
1927	15454	27068	1.20	2.5E-01	BE886804.1	EST_HUMAN	PM4-C10400-310700-005-008 C10400 Homo sapiens cDNA
2452	15019		12.03	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2538	15100	27073	0.93	2.5E-01	00798210	NT	<i>Mus musculus</i> protein-L-isocaspartate (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2540	15104		1.49	2.5E-01	AA251987.1	EST_HUMAN	zs111a12.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:6844822 5'
3459	16068		3.41	2.5E-01	AW973471.1	EST_HUMAN	EST385484 WAGE sequences, MAGM Homo sapiens cDNA
3587	16191	28675	0.84	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3603	16207	28685	7.97	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 29
4143	16735		1.36	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4409	16894		0.9	2.5E-01	Q03314	SWISSPROT	RIBB PROTEIN
4722	17303	29717	0.59	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-8 and 11-16
4880	17438		1.47	2.5E-01	Q27225	SWISSPROT	MOLT-4 INHIBITING HORMONE PRECURSOR (Mii-1)

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4869	17445	29898	4.69	2.5E-01	AF007768.1	NT	Charistomera fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4898	17471	29827	2.82	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4924	17499		3.21	2.5E-01	AJ230113.1	NT	Mus musculus armadil V gene, intron 4 segment containing 5'LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4959	17534	29878	0.61	2.5E-01	BE880785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5262	12633		0.65	2.5E-01	M28501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
5529	18161	30578	12.88	2.5E-01	SB83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6114	18730		0.84	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6738	18332	32138	0.83	2.5E-01	AJ251973.1	NT	Homo sapiens partial sterin-1 gene
7389	18814	32778	0.82	2.5E-01	U13892.1	NT	Feline calicivirus CFI/88 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	18838		1.35	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7632	20144	33025	4.48	2.5E-01	AL1631282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7788	20329	33236	2.31	2.5E-01	BF109040.1	EST_HUMAN	7157a03.1f Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7797	20340	33248	0.7	2.5E-01	BE860712.1	EST_HUMAN	601653391fR2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8168	20709	33625	2.2	2.5E-01	BF038595.1	EST_HUMAN	601456238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882809 5'
8338	20877	33798	0.72	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T ANTIGEN (E1B 18K)
8571	21110	34029	3.03	2.5E-01	HS3236.1	EST_HUMAN	X88407.1f Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
8808	21347	34271	0.88	2.5E-01	M886238.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21881	34909	15.88	2.5E-01	U889512	NT	Homo sapiens matrix metalloproteinase MMP_Ras-1 gene, promoter region
9435	21881	34910	15.98	2.5E-01	U889512	NT	Homo sapiens matrix metalloproteinase MMP_Ras-1 gene, promoter region
9492	21848	34897	2.09	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21848	34898	2.09	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35498	1.68	2.5E-01	AW581897.1	EST_HUMAN	RC3-ST188-130100-015-007 ST0188 Homo sapiens cDNA
10438	22830	35937	1.53	2.5E-01	AW152248.1	EST_HUMAN	xp40c10r1 NC1 CGAP_UH1 Homo sapiens cDNA clone IMAGE:2830034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
10439	22833	35941	1.31	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
10459	22853	35952	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22853	35953	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11172	24122	37153	5.29	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
11740	25075		10.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
579	13209	25887	1.87	2.4E-01	AA826316.1	EST_HUMAN	On70d4_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
881	13495	28014	2.4	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
1347	13642	28464	21.36	2.4E-01	AJ286880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTF1 gene	
1347	13642	28465	21.36	2.4E-01	AJ286880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTF1 gene	
1427	14020	28548	0.83	2.4E-01	Y17283.1	NT	Homo sapiens FLJ-1 gene, partial	
1891	14478		27.27	2.4E-01	AF287753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	
1844	14528	27084	1.17	2.4E-01	AF251708.1	NT	Zeocys dihumulatus fructosidase-1,8-bisphosphatase mRNA, complete cds	
2070	14689	27230	1.49	2.4E-01	AI742958.1	EST_HUMAN	wg7805.x1 Soenes_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:060267 OS0267 KIAA0512 PROTEIN .	
2183	14759	27329	1.04	2.4E-01	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes	
2213	14788		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)	
2302	14815	27451	1.78	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 100 of the complete genome	
2425	14893	27566	1.28	2.4E-01	BF002171.1	EST_HUMAN	Th22d04.x1 NCI_C3AP_Cof16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA O42588 26S PROTEASE REGULATORY SUBUNIT 6A .	
2575	15138	27708	3.05	2.4E-01	Z38534.1	NT	Discoidinum (Ax23-K) parA gene	
2790	15343	27913	1.70	2.4E-01	X71783.1	NT	S.pombe smf8 gene	
2812	15364	27933	3.88	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome	
3166	15780		3.27	2.4E-01	U72728.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (seq/poi) genes, complete cds	
3182	15795	28287	1.38	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PsiI fragment of intron 4	
3124	16325	28792	1.26	2.4E-01	AF169783.1	NT	Podospora amoenula HET-C protein (Het-c) gene, complete cds	
3824	18424	28986	0.83	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome	
4103	18687		0.6	2.4E-01	D28890.1	NT	Rattus norvegicus mRNA for alpha5 crystallin-related protein, complete cds	
5008	17581	30024	1.08	2.4E-01	AE000305.1	NT	Escherichia coli K-12 MG1655 section 185 of 400 of the complete genome	
5220	17785	30203	0.93	2.4E-01	BE737592.1	EST_HUMAN	6011572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839775.5	
5302	17884		1.55	2.4E-01	K02402.1	NT	Human coagulation factor IX gene, complete cds	
5653	18280	30758	0.83	2.4E-01	AB25707.1	EST_HUMAN	wg3305.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457129 3'	
5653	18280	30759	0.83	2.4E-01	AB25707.1	EST_HUMAN	wg3305.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457129 3'	
5676	18303	30785	0.85	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds	
5836	18460	31182	7.92	2.4E-01	AF089216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds	
5836	18460	31183	7.92	2.4E-01	AF089216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds	
8050	24754		1.02	2.4E-01	AI133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)	
8054	18872	31411	2.38	2.4E-01	BF582238.1	EST_HUMAN	7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPlicing Factor, Arginine/serine-rich 4 :contains element TAR1 TAR1 repetitive element	
8138	18752	31510	2.5	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18849	31619	2.28	2.4E-01	76818011	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6280	18898	31669	0.8	2.4E-01	AV733787	EST_HUMAN	AV733787 oda Homo sapiens cDNA clone oDADE115'
6856	18252	32055	2.43	2.4E-01	AI688389.1	EST_HUMAN	wc82c11.1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE_2323220 3' similar to gb:J03464
7381	18807	32772	8.84	2.4E-01	L48001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guac2) mRNA, complete cds
7708	20218	33108	1.08	2.4E-01	AF22844.1	NT	Mus musculus DXUm48s protein (DXUm48s) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ009397.1	NT	Streptococcus pneumoniae m08 and h08 genes; two component system 08
8139	20680	33592	0.71	2.4E-01	AJ009397.1	NT	Streptococcus pneumoniae m08 and h08 genes; two component system 08
8280	20831	33752	1.66	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila nucleolar gene encoding ribosomal protein L3, exons 1-2
8535	21074	33994	0.97	2.4E-01	BF242794.1	EST_HUMAN	601877879F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE_4108288 5'
8538	21127		0.58	2.4E-01	BF878275.1	EST_HUMAN	6020386188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE_4250372 5'
9059	21596	34528	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC1168 complete genome, segment 48
9059	21596	34527	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC1168 complete genome, segment 48
9482	21881	34826	6.84	2.4E-01	AI6883515.1	EST_HUMAN	wd43e02x1 Scareas_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE_2330806 3' similar to contains MER22b1 TAR1 repetitive element;
9820	22120	35083	0.8	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
9820	22120	35084	0.8	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10335	22829	35823	1.95	2.4E-01	Q03882	SWISSPROT	COLLAGEN ALPHA-1(X) CHAIN PRECURSOR
10847	23179	36192	3.25	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10715	23243	36260	2.9	2.4E-01	AF030189.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11081	23593		2.28	2.4E-01	ZZ1647.1	NT	P. asiatica mosaic virus genomic RNA
11685	24089	37145	1.91	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
11807	24853		2.65	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (ETL1) mRNA, complete cds
11868	24220		2.02	2.4E-01	AL278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12086	24838		2.18	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12320	25061		1.5	2.4E-01	BF220975.1	EST_HUMAN	RC3-CT0413-100800-0723-b06 CT0413 Homo sapiens cDNA
12562	24882		2.31	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
412	13047	25539	0.91	2.3E-01	S75898.1	NT	aromatase [Poophila guttata] in section 35 of 51 of the complete genome
685	13289		4.4	2.3E-01	U39713.1	NT	Mycobacteria genitalium in section 35 of 51 of the complete genome
695	13318	25803	17.02	2.3E-01	U67598.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
969	13580	26092	3.44	2.3E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE_3505818 5'
1847	14239	28774	1.19	2.3E-01	AD245480.1	NT	Brassica napus ssp. nigra gene for S-locus glycoprotein, cutiver T2
1874	14268	28800	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2089	14669		1.29	2.3E-01	AJ23533.1	NT	Homo sapiens partial intron 3 of the wild type Af-4/FEL gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15054	27628	2.03	2.3E-01	BE2B7718.1	EST_HUMAN	681175562F1 NIH_MGCC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2878	15238	27803	1.18	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2851	14024	28552	1.42	2.3E-01	AB016033.1	NT	Marinobufaglycidyl aglycone acts gnrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14857
							notfed08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element,contains element THR repetitive element;
2890	15808	28088	0.83	2.3E-01	AA601378.1	EST_HUMAN	Y211b07.s1 Scores, placenta Nb2-IP Homo sapiens cDNA clone IMAGE:1130357 3'
3120	15734		6.86	2.3E-01	R21732.1	EST_HUMAN	Y211b07.s1 Scores, placenta Nb2-IP Homo sapiens cDNA clone IMAGE:213283 5'
3417	18025	28507	0.78	2.3E-01	H69838.1	EST_HUMAN	Y97h10.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283
							GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3908	16507	28989	1.02	2.3E-01	S82821.1	NT	
4009	16807		5.14	2.3E-01	7862133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17028	29488	0.83	2.3E-01	R82522.1	EST_HUMAN	Y17f01.11 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:146017 5'
4489	17074		2.4	2.3E-01	L78788.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	29578	0.87	2.3E-01	D80888.1	NT	Synechocystis sp. PC-6803 complete genome, 1127, 1-133859
4586	17169	29813	2.16	2.3E-01	AF082255.1	NT	Homo sapiens mitogen-activated protein kinase p38-beta (PRKMK13) mRNA, complete cds
4652	17234	29890	6.13	2.3E-01	5031984	NT	Homo sapiens nucleic transport factor 2 (placental protein 15) (PP15) mRNA
5180	17585	30028	0.62	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17767	30191	0.62	2.3E-01	AB03240.1	NT	Mus musculus tulp 1 mRNA, complete cds
5403	17981	30372	0.9	2.3E-01	AE002240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB04045.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
							7k3b06.s1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW.GAG_SMSAV P03330 GAG POLYPEPTIDE (CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10);
6621	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	C.familiaris rsm1 gene
5721	18347	31050	4.93	2.3E-01	X85587.1	NT	Vitafoma cornuta small subunit ribosomal RNA gene
5831	18455		1.19	2.3E-01	L39112.1	NT	23S rRNA [Leucostomat camosum, Genomic, 2808 nt]
6926	18548	31274	0.78	2.3E-01	S80377.1	NT	6827612.s1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6098	18712	31481	2.34	2.3E-01	AI708840.1	EST_HUMAN	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							6827612.s1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6762	18355	32164	0.78	2.3E-01	AF198089.1	EST_HUMAN	Cytoblasta cuticular cytochrome oxidase subunit Vta (coxV42) mRNA, complete cds; nuclear gene for mitochondrial product
6859	19538	32280	4.1	2.3E-01	AI718148.1	EST_HUMAN	684212.s1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element,
7165	19897	32544	0.7	2.3E-01	8822323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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7331	18858	32721	0.69	2.3E-01	AF000227.1	NT	Sacale cereale omega secalin gene, complete cds
7445	18869	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein Lm17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32898	1.63	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE_3912859 5'
7732	20240		2.68	2.3E-01	N80803.1	EST_HUMAN	za12a08_L1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE_2892358 5'
7783	20336	33243	0.58	2.3E-01	AL161558.2	NT	Anabiodopsista italiana DNA chromosome 4, contig fragment No. 58
7835	20477	33387	1.93	2.3E-01	M88631.1	NT	Oxytricha nova macrotusker telomere-binding protein alpha subunit (tet-alpha alanine version) gene, complete cds
8430	20870	33882	0.6	2.3E-01	U57889.1	NT	Mus musculus prosoposin (pspp)GP-1 gene, complete cds
9067	21804	34534	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to Dm11 homolog (GB>J083388)
9067	21804	34535	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to Dm11 homolog (GB>J083388)
9501	22001	34958	0.65	2.3E-01	6678318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
9844	22144	35112	0.51	2.3E-01	BE277880.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE_2888739 5'
9897	22198	35169	0.78	2.3E-01	AWB64460.1	EST_HUMAN	EST3786533 MAGE sequences, MAGH Homo sapiens cDNA
9746	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 3.1.21.4))
9781	22279	35284	0.55	2.3E-01	AW384633.1	EST_HUMAN	PM2-DT0036-281209-001-f04 DT0036 Homo sapiens cDNA
9847	22345	35326	2.6	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
9903	22400	35373	1.83	2.3E-01	A1293281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35820	0.94	2.3E-01	AF201929.1	NT	Marine hepatitis virus strain 2, complete genome
10351	22845		5.88	2.3E-01	BF133577.1	EST_HUMAN	601848115SF2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE_4102082 3'
10883	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10883	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11068	23580	36819	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11068	23580	36820	1.85	2.3E-01	AJ250188.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11220	23761	36817	2.49	2.2E-01	AE002187.2	NT	Chlamydomonas pneumoniae AR39, section 4 of 94 of the complete genome
11624	24068		1.6	2.3E-01	AV709738.1	EST_HUMAN	AV709738 ADC Homo sapiens cDNA clone ADCAHG101 5'
11788	24172		2.82	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11878	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST744 HT28M8 Homo sapiens cDNA clone HCoE44 5'
11899	24804		1.31	2.3E-01	AA088819.1	EST_HUMAN	chn124.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11903	24240		1.61	2.3E-01	AW863840.1	EST_HUMAN	PMA-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA
11989	25002	30610	3.1	2.3E-01	AW303623.1	EST_HUMAN	xw21d07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE_2813773 3' similar to TRQ982175 Q9Z175 LYSM_OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;

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12007	25053	30511	10.98	2.3E-01	BE88264.1	EST_HUMAN	NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12057	24340		1.94	2.3E-01	BF063318.1	EST_HUMAN	NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5'
12107	24289		3.11	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U49845.1	NT	Pleurodes wall distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ005619.1	NT	Rattus norvegicus mRNA for acid gated ion channel IMAGE:3395950 3' similar to contains element nac3gh12.21 LypsdI static_nerve Homo sapiens cDNA clone IMAGE:1675280 3' similar to MER38 repetitive element;
12480	24614		2.57	2.3E-01	BF478611.1	EST_HUMAN	lambda ZAP Express. Homo sapiens cDNA clone IMAGE:1675280 3' similar to
12988	24888	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	cl1834.seq.F Human fetal heart, Lambda ZAP Express. Homo sapiens cDNA 5'
83	12789	25252	0.91	2.2E-01	AI062190.1	EST_HUMAN	oxf14a10.41 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
1611	14204	25738	2.85	2.2E-01	AF187650.1	NT	Homo sapiens PPARG delta gene, promoter region
2063	14643		3.89	2.2E-01	AF171601.1	NT	Trimemurus mitchellicus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2138	14714	27287	3.16	2.2E-01	NR4840.1	NT	Fresh-water sponge Eumetaphyllum alpha collagen (COLF1) gene
2447	15014	27588	6.61	2.2E-01	BF977398.1	EST_HUMAN	NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
26223	15185	27751	1.27	2.2E-01	BE016258.1	EST_HUMAN	NIH_MGC_87 Homo sapiens cDNA clone IMAGE:38868190 5'
26223	15185	27752	1.27	2.2E-01	BE618258.1	EST_HUMAN	NIH_MGC_87 Homo sapiens cDNA clone IMAGE:38868190 5'
2703	15280		1.17	2.2E-01	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
28008	15523	27983	4.28	2.2E-01	BE155255.1	EST_HUMAN	PM2-HT0353-281288-003-e12 HT0353 Homo sapiens cDNA
28008	15523	27984	4.28	2.2E-01	BE155255.1	EST_HUMAN	PM2-HT0353-281288-003-e12 HT0353 Homo sapiens cDNA
2947	15583		1.84	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3439	16047		2.87	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
38886	16484		1.18	2.2E-01	AF165728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
42811	16817		1.28	2.2E-01	AF118102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4300	16886	26030	7.03	2.2E-01	AF155142.1	NT	Mus musculus mitotic lineage kinase 3 (Mll3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4350	16937	26378	2.59	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4350	16937	26379	2.59	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4447	17033	26475	1.36	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4447	17033	26476	1.36	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4952	17527		1.35	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4957	17532	26974	2.88	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.1 Strategene NNT neuron (#537233) Homo sapiens cDNA clone IMAGE:6489688 5'
6198	17781		1.33	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5203	17788		1.78	2.2E-01	AE001197.1	NT	Borrelia burgdorferi (section 23 of 70) of the complete genome

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5281	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0087-201089-002-e10 HT0087 Homo sapiens cDNA
6316	17878		0.9	2.2E-01	S57585.1	NT	histamine H2-receptor [rats, Generic, 1828 nt]
5919	18541	31287	2.4E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA	
5930	18552		3.53	2.2E-01	DB4000.1	NT	Synechozytis sp. PCG8803 complete genome, 1827, 2392738-2538889
6150	18763	31525	0.73	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tox1) mRNA, complete cds
6150	18763	31526	0.73	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tox1) mRNA, complete cds
6807	19398	32212	0.85	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7083	19684	32533	9.14	2.2E-01	AV758298.1	EST_HUMAN	AV758298 BM Homo sapiens cDNA clone BMFAHC08 5'
7183	19715	32502	1.48	2.2E-01	AF082758.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spa) genes, complete cds; and unknown genes
7183	19716	32583	1.48	2.2E-01	AF082758.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spa) genes, complete cds; and unknown genes
7333	18860	32723	2.01	2.2E-01	M24138.1	NT	Human glycoprotein B gene, exon 4
7333	18860	32724	2.01	2.2E-01	M24138.1	NT	Human glycoprotein B gene, exon 4
							Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B3 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7688	20197	33085	0.68	2.2E-01	AF287987.1	NT	
7863	20505		3.08	2.2E-01	AF155143.1	NT	Mus musculus nm23-H11 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z48833.1	NT	E.coli sepA and sepB genes
8815	21354	34277	0.67	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21388	34290	3.48	2.2E-01	AE001713.1	NT	Thermitobius maritima section 25 of 138 of the complete genome
8847	21389	34310	1.02	2.2E-01	U08864.1	NT	
8852	21490		3.12	2.2E-01	AW856039.1	EST_HUMAN	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8943	21580	34509	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Deaf1), mRNA
9128	21681	34604	1.95	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110800-038-c02 TN0045 Homo sapiens cDNA
9213	21730	34673	1.24	2.2E-01	W02888.1	EST_HUMAN	ZB04108.1 Scores melanocyte 2N1HM Homo sapiens cDNA clone IMAGE-231591 5'
9221	21653	34903	14.03	2.2E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21800	34750	0.74	2.2E-01	AJ008838.1	NT	Xenopus laevis mRNA for kinasin-like protein 3 (Xkps)
9285	21895	34830	0.71	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9288	21898	34845	3.69	2.2E-01	M89643.1	NT	Brachyhyaline ratio epoxide ring beta and gamma chains (Epdr) gene, complete cds
8839	22039	35000	0.59	2.2E-01	Q803890	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor		
9729	222277	35204	3.1	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSVP21) mRNA, complete cds; nuclear gene for chloroplast product		
98854	22381	35341	2.23	2.2E-01	BF206507.1	EST_HUMAN	601888724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100188 5'		
10079	22574	35598	0.87	2.2E-01	9825671	NT	Human herpesvirus 5, complete genome		
10340	22834	0.81	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Pph1) gene, partial cds			
10384	22878	35870	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome		
10384	22878	35871	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome		
11005	23519	38554	1.6	2.2E-01	AF257722.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced		
11299	23751	38888	5.58	2.2E-01	X0198.1	NT	Drosophila 68C glue gene cluster		
11335	23033	38942	3.18	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA		
11715	24125		1.8	2.2E-01	BE870859.1	EST_HUMAN	601446857F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850670 5'		
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A3 (MAGEA3), cathepsin (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathepsin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1 ^a		
11827	25035		8.34	2.2E-01	U826712	NT			
11910	24248		5.37	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds		
12024	18020	30461	1.7	2.2E-01	AW381098.1	EST_HUMAN	RC1-CTD249-141188-021-004 CT02649 Homo sapiens cDNA		
12026	24317		1.85	2.2E-01	AW681822.1	EST_HUMAN	HR76022R1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'		
12575	25058		4.05	2.2E-01	AV894801.1	EST_HUMAN	AV894801 GKC Homo sapiens cDNA clone GKCAHB02 5'		
12659	24730	30855	2.44	2.2E-01	BF243095.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104888 5'		
1038	13817	28132	1.38	2.1E-01	AA569289.1	EST_HUMAN	mm31@11.1st NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804		
1038	13819	28134	1.27	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16		
1163	13785		2.41	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome		
1240	13838	28354	0.85	2.1E-01	6754288	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA		
1240	13839	28355	0.85	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA		
1557	14149	28881	3.45	2.1E-01	AJ240805.1	NT	Mus musculus proto-oncogene and Igf2r gene for Insulin-like growth factor type 2 and L41ps and Au76 pseudogenes		
1857	14541	27067	1.84	2.1E-01	AA900824.1	EST_HUMAN	ck73022.51 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02785 COMPLEMENT C3 PRECURSOR (HUMAN)		
2201	14777	27350	3.39	2.1E-01	BF0865073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'		
2385	14954	27626	2.01	2.1E-01	6753235	NT	Mus musculus calcium channel, voltage dependent, alpha2delta subunit 3 (Caeme233), mRNA		
2851	15587	28041	2.63	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA		
3879	16477		6.58	2.1E-01	6838361	NT	Beta vimentin mRNA		
4120	16721	28178	1.22	2.1E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180		

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Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4128	16721	20177	1.22	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4338	168223		1.38	2.1E-01	AF124528.1	NT	Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4465	17051		1.51	2.1E-01	AB03041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4676	17258	20709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens psip47 gene, complete cds
5083	17656	30097	1.83	2.1E-01	U78498.1	NT	Lycopetanin esculentum homoeobox 1 protein (THox1) mRNA, partial cds
5434	17890	30396	0.88	2.1E-01	J05082.1	NT	Vampiro bat (<i>D. rotundus</i>) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF672895.1	EST_HUMAN	6021520171 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:42830015'
6897	18544	32368	1.16	2.1E-01	AJ223392.1	NT	Doto fragilis mitochondrial 16S rRNA gene, partial
6898	18477	32289	2.04	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7438	18890	32825	1.24	2.1E-01	Q01858	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7438	18890	32826	1.24	2.1E-01	Q01858	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7447	18971		2.17	2.1E-01	AE000872.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Carts familiaris keratin (KRT9) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF086887.1	NT	Glycine max malate dehydrogenase (MdH-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF086887.1	NT	Glycine max malate dehydrogenase (MdH-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7765	20273		0.68	2.1E-01	T87554.1	EST_HUMAN	yd83b01.r1 Scores fetal liver spleen 1NFLS_Homo sapiens cDNA clone IMAGE:114793 5'
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8439	20979	33894	4.93	2.1E-01	U68398.1	NT	Haemophilus influenzae hmcD, putative haemocidin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocidin structural protein (hmcA), and haemocidin immunity protein (hmcI) genes, complete cds
8732	21271	34190	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hb83) Homo sapiens cDNA clone DKFZp434H0814 5'
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hb83) Homo sapiens cDNA clone DKFZp434H0814 5'
8898	21428		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APCL gene, exon 9
8897	21505	34428	5.93	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL022W
9423	21932	34880	0.6	2.1E-01	N42538.1	EST_HUMAN	yy11e10_r1 Scores melanocyte 2Nb1-M Homo sapiens cDNA clone IMAGE:270954 5'
9423	21932	34881	0.6	2.1E-01	N42538.1	EST_HUMAN	yy11e10_r1 Scores melanocyte 2Nb1-M Homo sapiens cDNA clone IMAGE:270954 5'
9432	21958	34906	2.95	2.1E-01	X97278.1	NT	<i>A.thaliana</i> mRNA for ARRnBP1b protein
9538	22036	34996	1.57	2.1E-01	AB030529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10232	22727	35719	1.04	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10283	22758						DIACYL GLYCEROL KINASE, DELTA (DIGLYCEROL KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10289	22784	35751	1.98	2.1E-01	P52824	SWISSPROT	(80 kD DIACYL GLYCEROL KINASE)
			0.67	2.1E-01	BF574254.1	EST_HUMAN	6021314271 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10505 22899	36007		0.5	2.1E-01	AF294286.1	NT	Anolis lineatopus isoleucine NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11438 23888			2.24	2.1E-01	11036847	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451 23901	36969		2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0822-040500-013-b11 HT0822 Homo sapiens cDNA Drosophila melanogaster ALA-E6 DNA, repeat region
11841 24802			1.39	2.1E-01	X57824.1	NT	Homo sapiens fragile 16D cathe reductase (FOR) gene exons 8, 9, and partial cds IMAGE:3915675_5'
12183 24418			1.46	2.1E-01	AF217490.1	NT	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3222034_3'
12465 24593			1.72	2.1E-01	BE622249.1	EST_HUMAN	7e59e02x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3222034_3'
12807 24891	30858		2.08	2.1E-01	BE072230.1	EST_HUMAN	Mus musculus genomic fragment, 279 Kb, chromosome 7
12812 24895	30861		1.28	2.1E-01	AJ276865.1	NT	Gelius galius mRNA for avian, complete cds
214 12875	25362		1.88	2.0E-01	AB017437.1	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
559 13190			2.22	2.0E-01	7705601	NT	O. caniculus gammeline IgH heavy chain V-H pseudogene, alleotype VHα2
728 13348	25840		1.24	2.0E-01	MT7083.1	NT	Mus musculus Major Histocompatibility Locus class II region
843 13459	25968		1.78	2.0E-01	AF027885.1	NT	Synochocystis sp. PCe8683 complete genome, 7127_781449_0200916
1049 13886	28167		0.72	2.0E-01	D90905.1	NT	Homo sapiens chromosome 21 segment HS21C013
1164 13798	28276		3.24	2.0E-01	AL163213.2	NT	Homo sapiens rac1 gene
1287 13891	28414		1.37	2.0E-01	AL132895.5	NT	Plum pox virus strain M, complete genome, isolate PS
1351 13948	28470		1.22	2.0E-01	AW384837.1	EST_HUMAN	PML-HT0422-291-299-002-d08 HT0422 Homo sapiens cDNA
1507 14099			1.22	2.0E-01	AJ243857.1	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1534 14126	28683		23.08	2.0E-01	4503408	NT	Homocysteic acid synthetase 1 specific transcript KIAA0505
1569 14191	28722		3.03	2.0E-01	AB007974.1	NT	Human bradykinin B1 receptor (brackb1) gene, complete cds
1604 14198	28728		1.23	2.0E-01	AF280700.1	NT	Homocysteic acid synthetase 1 specific transcript KIAA0505
1735 14326	28858		1.17	2.0E-01	U22348.1	NT	Homocysteic acid synthetase 1 specific transcript KIAA0505
1755 14345			1.83	2.0E-01	AF111170.3	NT	Homocysteic acid synthetase 1 specific transcript KIAA0505
1785 14385			1.98	2.0E-01	U67525.1	NT	Homocysteic acid synthetase 1 specific transcript KIAA0505
1824 14518	27073		1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330_5'
1824 14518	27074		1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330_5'
1837 14521	27077		1	2.0E-01	89222238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
23886 14855			1.64	2.0E-01	X82877.1	NT	H.sapiens Net-D-Glucosidase cotransport regulator gene
2915 15532			0.88	2.0E-01	AF074280.1	NT	Homeobox full length Insert cDNA YH85A11
3534 16139	28621		0.7	2.0E-01	P46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZP PROTEIN ATHB-10)
3629 16229			0.82	2.0E-01	AW238005.1	EST_HUMAN	MER21 repetitive element:
3788 16389	28535		0.8	2.0E-01	P34841	SWISSPROT	CED-11 PROTEIN

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Probe Seq ID No:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	18826	28098	0.78	2.0E-01	Z46906.1	NT	Sus scrofa
4102	18838	29152	0.68	2.0E-01	X83887.1	NT	C.parasitica espC gene
4522	17108	28552	0.78	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nrip6) gene, complete cds; and Nrip3 gene, exons 2-9 and 11-18
4885	17247		8.43	2.0E-01	BE820165.1	EST_HUMAN	QV4-EN0032-180500-223-003 Homo sapiens cDNA
5182	17757	30188	7.09	2.0E-01	88922030.0	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5226	16139	28621	0.62	2.0E-01	P46907	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5838	18285	30737	2.38	2.0E-01	X5680.0.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5916	18838	31283	2	2.0E-01	114292540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6008	18826	31361	0.69	2.0E-01	X91856.1	NT	F-nutriplex DNA encoding for very t-RNA synthetase
6210	18820	31591	0.48	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Haf5p (HAL5) mRNA, complete cds
6321	18828		0.71	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6560	19158	31855	3.94	2.0E-01	X61033.1	NT	M.sauritus mu class glutathione transferase gene
6850	18246	32049	3.63	2.0E-01	AW380865.1	EST_HUMAN	PM1-CT0247-141098-001-008 CT0247/Homo sapiens cDNA
7251	19780	32838	0.68	2.0E-01	U39724.1	NT	Mycobacteria genitalium section 48 of 51 of the complete genome
7336	18883	32727	1.18	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pflic) gene, exons 3 through 7
7775	20284	33181	1.53	2.0E-01	AK024427.1	NT	Homo sapiens mRNA for FLJ09016 protein, partial cds
7895	20437		6.45	2.0E-01	AF028028.1	NT	Andes virus strain OK23133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20883	33595	2.91	2.0E-01	X91161.1	NT	M.musculus sop2 gene exon 14
8858	21197		0.53	2.0E-01	BE562247.1	EST_HUMAN	601344648F1 NIH_MGC_8_Homo sapiens cDNA clone IMAGE:3677794_5
9273	21708	34749	1.03	2.0E-01	U82511.1	NT	Dichotomium discoidatum random slug cDNA 19 protein (rsc19) mRNA, partial cds
9312	21828	34775	0.65	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9475	21874		4.35	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 37 of the complete genome
9881	22160	35132	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9881	22160	35133	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9898	22304		1.98	2.0E-01	AF148692.1	NT	Homo sapiens flamin 2 (FLN2) mRNA, complete cds
9894	22449	35431	1.79	2.0E-01	AF088007.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9854	22449	35432	1.79	2.0E-01	AF088007.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10072	22587	35562	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22587	35563	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22810		0.72	2.0E-01	X78238.1	NT	D.melanogaster DNA mobile element (happel)
10304	22788	35769	0.88	2.0E-01	X87121.1	NT	R.norvegicus mRNA for NTR2 receptor
10720	23248	36263	2.77	2.0E-01	D89088.1	NT	Satellinus planius mRNA for transferrin, complete cds

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10720	23248	36284	2.77	2.0E-01	D8908B.1	NT	Schelinus pluvius mRNA for transferrin, complete cds
12162	24402		1.34	2.0E-01	AF206837.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF902773.1	NT	Homo sapiens minirh-Lm isoform (minirh) mRNA, complete cds
12388	24807	30788	2.81	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12423	24610	30888	3.97	2.0E-01	AJ023592.1	EST_HUMAN	or86bar10_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12449	24584		17.08	2.0E-01	AF078184.2	NT	Homo sapiens Kif70-binding protein (KUB3) mRNA, partial cds
1115	12786		6.22	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
374	13023	25569	5.4	1.9E-01	AF004353.1	NT	Mus musculus plate car (pc) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.9E-01	U325812	NT	Homo sapiens lambdoidoda protein kinase C-interacting protein mRNA, complete cds
684	13308	25783	1.47	1.9E-01	U325812	NT	Homo sapiens lambdoidoda protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.6	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-01-d01 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-01-d01 BT0502 Homo sapiens cDNA
1023	13833		1.92	1.9E-01	7305190	NT	Mus musculus interferon 2 receptor, gamma chain (IFNg), mRNA
1143	13748	26258	10.04	1.8E-01	AA358813.1	EST_HUMAN	EST87734 fetal lung II Homo sapiens cDNA 5' end
1413	14008	28534	2.41	1.8E-01	AF081282.1	NT	Sorghum bicolor 22 kDa leftrin cluster
1482	14075		4.02	1.8E-01	AF184623.1	NT	Plasmidium wakayamycotoxine binding protein-2 (rbp-2) gene, complete cds
2185	14761	27331	1.29	1.8E-01	AA810482.1	EST_HUMAN	Q44H09_s1 Soares_NFL_I_G8C_S1 Homo sapiens cDNA clone IMAGE:15263369 3' similar to gb:AF03811
2422	14930	27583	3.27	1.8E-01	8922533	NT	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2849	15565	28039	4.1	1.8E-01	U68068.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2865	15580		6.58	1.8E-01	J00922.1	NT	Sigmodon hispidus p53 gene, partial cds
3033	15640	28128	1.05	1.8E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBM) mRNA, partial cds
3442	16050	28528	4.19	1.8E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3528	16131	28511	5.24	1.8E-01	R16467.1	EST_HUMAN	Y42F10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3877	18475	28539	0.78	1.8E-01	AF264017.1	NT	Rattus norvegicus myoactin mRNA, complete cds
4084	16661	29123	3.85	1.8E-01	AB008784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4157	16749	29202	1.86	1.8E-01	AW754108.1	EST_HUMAN	CN3-CT0315-271198-045-b11 CT0315 Homo sapiens cDNA
4315	16901	29345	1.17	1.8E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4568	17161	29597	0.69	1.8E-01	AL161482.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5158	17728		1.11	1.8E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5789	18414		5.46	1.8E-01	AW130149.1	EST_HUMAN	X728a07_x1 NCI_CGAP_UM Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb:MT3778 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5828	18450	31173	7.81	1.8E-01	AF127837.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6005	18625	31360	0.73	1.8E-01	AF080216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046 18885				2.52	1.8E-01 AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001928 5'
6489 19070		31853		1.07	1.8E-01 AI762391.1	EST_HUMAN	W54H02X1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:23844089 3'
6823 19123		31915		1.23	1.8E-01 AW148452.1	EST_HUMAN	Xf14608.X1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050 18889		30460		1.37	1.8E-01 IR43212.1	EST_HUMAN	Yg0an12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31983 3' similar to contains MER13 repetitive element;
7072 18844		32481		0.91	1.8E-01 AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 8-11
7072 18844		32482		0.91	1.8E-01 AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 8-11
7503 20025		32889		1.3	1.8E-01 U80822.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP6) gene, complete cds
7543 20083		32837		2.89	1.8E-01 AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
7827 20488		33378		1.71	1.8E-01 AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8820 21159		34074		12.12	1.8E-01 AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8875 21414		34337		1.36	1.8E-01 M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8875 21414		34338		1.36	1.8E-01 M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9789 22287		35271		0.72	1.8E-01 AA912486.1	EST_HUMAN	ab69g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537508 3' similar to contains Atu repetitive element;
10140 22835		35628		0.71	1.8E-01 BE830353.1	EST_HUMAN	RCS-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
10140 22835		35627		0.71	1.8E-01 BE830353.1	EST_HUMAN	RCS-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
10523 23081		38071		2.02	1.8E-01 AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523 23081		38072		2.02	1.8E-01 AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10635 23187		38178		2.08	1.8E-01 AF2223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11337 23829		36891		1.68	1.8E-01 M22253.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
11571 24018		37088		2.69	1.8E-01 AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207 24431				1.33	1.8E-01 AF056900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582 24974				3.69	1.8E-01 AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34 12713		25172		2.58	1.8E-01 U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
281 15412		25423		1.67	1.8E-01 AB022080.1	NT	Mus musculus Cctg gene for chaperon containing TCP-1 gamma subunit, partial cds
393 13039		25530		1.76	1.8E-01 4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
776 13395		25898		0.77	1.8E-01 AB021490.2	NT	Oryza latifolia gene for membrane guanylyl cyclase OIGC1, complete cds
1018 13528		28141		0.78	1.8E-01 AI912212.1	EST_HUMAN	W67102X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130 13732		28242		1.28	1.8E-01 AF000580.1	NT	Dichotomella discoidatum plasmid Ddp5, complete genome
1332 13928		28447		6.97	1.8E-01 AL117189.1	NT	Yersinia pestis plasmid pCD1

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Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1551	14143	28878	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	28877	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA gg22d10_5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O76838 O76838
1907	14492		2.22	1.8E-01	AI733708.1	EST_HUMAN	GAMMA BUTYROBETANE HYDROXYLASE :
1958	14542	27088		1.52	1.8E-01	AB051987.1	NT
27118	15273		2.28	1.8E-01	AW825728.1	EST_HUMAN	Mus musculus Scy68, Scy69, Scy616-ps, Scy65 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scy16 pseudogene, small inducible cytokine A5 precursor, complete cds
28223	15540		2.38	1.8E-01	AF194589.1	NT	Jonopsidium aculeae LEAFY protein (LEAFY2) gene, partial cds
28228	15544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	H411633.x1 Soenes_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2858758 3'
3158	15772	28239	1.31	1.8E-01	AW885178.1	EST_HUMAN	QV0-BN0041-070300-147-004 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF182852.1	EST_HUMAN	Y45601.x1 Soenes placenta Nb2-hIP NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3683	16284	28752	0.79	1.8E-01	HO3369.1	EST_HUMAN	Y45601.x1 Soenes placenta Nb2-hIP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Ala repetitive element
3683	16284	28753	0.79	1.8E-01	HO3369.1	EST_HUMAN	Y45601.x1 Soenes placenta Nb2-hIP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Ala repetitive element
4333	16920	28362	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudobasal region; segment 1/2
44238	17012		4.07	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BdA-DCB), complete cds
4654	17226	28891	6.56	1.8E-01	AL161598.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
4888	17481	28914	2.51	1.8E-01	AB051987.1	NT	Mus musculus Scy68, Scy69, Scy616-ps, Scy65 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scy16 pseudogene, small inducible cytokine A5 precursor, complete cds
49228	17503	28950	1.03	1.8E-01	X82179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
5198	17703		2.18	1.8E-01	AW812270.1	EST_HUMAN	MR3-ST10203-151288-112-908 ST10203 Homo sapiens cDNA
5216	17701	30200	1.59	1.8E-01	AI792382.1	EST_HUMAN	an28g07_x5 Geissler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5257	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Ne-taurocholate cotransporting polypeptide mRNA, partial cds
5281	17833	30270	1.07	1.8E-01	AI439881.1	EST_HUMAN	Y57604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5289	17850	30276	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17889	30314	0.78	1.8E-01	AJ132844.1	NT	Broad beam with virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17889	30315	0.78	1.8E-01	AJ132844.1	NT	Broad beam with virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17856	30367	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST10121-041188-019-b01 ST10121 Homo sapiens cDNA

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Table 4
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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5978	18596	31331		1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 80
6082	18889	31446	1.01	1.8E-01	N28829.1	EST_HUMAN	Scorpio.1 Scores melanocyte 21bHIM Homo sapiens cDNA clone IMAGE:284063 5
6277	18885	31653	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA
6277	18885	31654	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA
6635	18231	32035	2.03	1.8E-01	Q8CYY4	SWISSPROT	FORKHEAD BOX PROTEIN E3
6675	18271		2.24	1.8E-01	N84853.1	EST_HUMAN	yy62h02/1 Scores_multiple_sclerosis_21bHMSP Homo sapiens cDNA clone IMAGE:278163 5
7077	18649	32487	1.22	1.8E-01	AB018561.1	NT	Citellus lemnatus mRNA for wsus, complete cds
7077	19849	32488	1.22	1.8E-01	AB018561.1	NT	Citellus lemnatus mRNA for wsus, complete cds
7117	19457	32272	0.71	1.8E-01	BE891353.1	EST_HUMAN	60164838TR2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:38922417 3
8547	21088	34099	0.47	1.8E-01	AW860118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI1 Homo sapiens cDNA
9288	21782	34741	1.13	-	M73258.1	NT	Human cellular DNA/human papillomavirus proximal DNA
9288	21886	34843	1.39	1.8E-01	9826232	NT	Bacteriophage lke, complete genome
9412	21821		0.55	1.8E-01	AA483751.1	EST_HUMAN	nh02605.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:243088 similar to contains L1.13 L1 repetitive element;
9494	21894	34950	1.13	1.8E-01	PI5272	SWISSPROT	AMP NUCLEOSIDASE
9494	21894	34951	1.13	1.8E-01	PI5272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34950	0.85	1.8E-01	M28019.1	NT	S.commu arachidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9532	22032	34951	0.85	1.8E-01	M28019.1	NT	S.commu arachidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9694	22193	35168	0.62	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHAN ALPHA 2(1) CHAIN PRECURSOR
9698	22197	35170	0.69	1.8E-01	U57548.1	NT	Methanococcus jannaschii section 80 of 150 of the complete genome
10039	22534		0.64	1.8E-01	AF202052.1	NT	Aquarius simplex cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial product
10271	22763	35753	1.22	1.8E-01	X83440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10516	23054	36008	2.37	1.8E-01	X77338.1	NT	Archaea mRNA for ribonucleotide reductase R2
10558	23094	36106	7.47	1.8E-01	U83606.1	NT	Bacteriophage r1 integrase, repressor protein (rro), dUTPase, holin and lysozyme, complete cds
10615	19849	32487	3.07	1.8E-01	AB018561.1	NT	Citellus lemnatus mRNA for wsus, complete cds
10616	19849	32488	3.07	1.8E-01	AB018561.1	NT	Citellus lemnatus mRNA for wsus, complete cds
10616	23148	38190	4.49	1.8E-01	AF019107.1	NT	Dicytostelium discoideum unknown (DG1041) gene, complete cds
10897	23417	38434	1.84	1.8E-01	M58227.1	NT	Human carcinocembryonic antigen (CEA) gene, exon 4
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11588	24042	37111	2.74	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Txba2r), mRNA
11628	24068	37132	1.6	1.8E-01	U40487.1	NT	Mycoplasma smegmatis proton antiporter efflux pump (MraA), complete cds
11748	24148		2.04	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11814	24188	31032	1.41	1.E-01	BF34823.1	EST_HUMAN	602019028F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12218	13826	28447	1.3	1.E-01	AL117189.1	NT	<i>Yersinia pestis</i> plasmid pCD1
12291	24491		5.61	1.E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN)(PTP PROTEIN)
12418	24589		23.47	1.E-01	R24494.1	EST_HUMAN	Y48h10.11 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24580		2.75	1.E-01	Y11114.1	NT	<i>E.coli</i> disper mRNA for heat shock protein (hsc1)
12502	25045	30507	1.58	1.E-01	9506852	NT	<i>Rattus norvegicus</i> procollagen C-proteinase enhancer protein (Pcode), mRNA
603	13232	25705	6.53	1.E-01	BE985164.1	EST_HUMAN	601274804F1 NIH_WGC_20 Homo sapiens cDNA clone IMAGE:3815788 5'
838	13454	25884	2.89	1.E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
886	13688		8.63	1.E-01	P35216	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE)(NF-L)
1098	13701	26210	0.97	1.E-01	AF081810.1	NT	<i>Lymnaea disper</i> nucleopolyhedrovirus, complete genome
1096	13701	26211	0.97	1.E-01	AF081810.1	NT	<i>Lymnaea disper</i> nucleopolyhedrovirus, complete genome
1853	14441	26898	0.93	1.E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2025	14807		2.84	1.E-01	AF255051.1	NT	<i>Homo sapiens</i> BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2885	15503	27973	1.98	1.E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hypR) gene, partial cds; <i>hemagglutinin</i> protease regulatory protein (hypR) gene, complete cds; and YRAL_VIBCO gene, partial cds
2885	15503	27974	1.98	1.E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hypR) gene, partial cds; <i>hemagglutinin</i> protease regulatory protein (hypR) gene, complete cds; and YRAL_VIBCO gene, partial cds
2885	15503	28044	1.53	1.E-01	AA336808.1	EST_HUMAN	EST41851 Endometrial tumor Homo sapiens cDNA 5' end
3027	15643	28121	1.9	1.E-01	AJ238738.1	NT	<i>Naja naja</i> atra cdv-1 gene, exons 1-3
3027	15643	28122	1.9	1.E-01	AJ238738.1	NT	<i>Naja naja</i> atra cdv-1 gene, exons 1-3
3139	15753	28220	1.91	1.E-01	AF081514.1	NT	Tacca canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3412	16020	28500	1.11	1.E-01	NS5763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3404	16099	28574	1.28	1.E-01	AJ288505.1	NT	<i>Anabena</i> sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4012	16610	28683	4.89	1.E-01	AJ235377.1	NT	<i>Homo sapiens</i> derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4658	17240		1.63	1.E-01	X52835.1	NT	Schistocerca gregaria alpha repetitive DNA
4877	17452	28604	0.84	1.E-01	AF217480.1	NT	<i>Homo sapiens</i> fragile XSD codio reductase (FOR) gene, exons 8, 9, and partial cds
4885	17539	28891	1.07	1.E-01	AJ247835.1	EST_HUMAN	qh576081X1 Scores_fetal_liver_spoken_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 5' similar to contains OFR.b1 OFR repetitive element;
5210	17775		0.88	1.E-01	U28378.1	NT	Zea mays calcium-dependent protein kinase (ZMECDP2) mRNA, complete cds
5242	17808	30227	1.02	1.E-01	BF889719.1	EST_HUMAN	60218863OF1 NIH_WGC_49 Homo sapiens cDNA clone IMAGE:4288846 5'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5287 178559			1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ze) gene, complete cds
5342 17003	30319	0.6	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'	
5421 17878	30398	7.82	1.7E-01	J04479.1	NT	S_pneumoniae DNA polymerase I (pol) gene, complete cds	
5604 18233	30683	1.92	1.7E-01	AA470688.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:8810688 3' similar to gb:M17888 60S	
5604 18233	30684	1.92	1.7E-01	AA470688.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	
5778 18404	31120	0.7	1.7E-01	U43589.1	NT	Brugia palliata microfilarial sheath protein SHP-3 (shp3) gene, complete cds	
6471 18072	31858	20.9	1.7E-01	H72118.1	EST_HUMAN	ys02c9a8.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213858 3'	
6522 18122	31913	1.33	1.7E-01	AI376978.1	EST_HUMAN	te28c11.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'	
6522 18122	31914	1.33	1.7E-01	AI376978.1	EST_HUMAN	te28c11.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'	
6937 18045	30487	0.71	1.7E-01	BE300288.1	EST_HUMAN	60094406771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'	
6960 18837			2.28	1.7E-01	AF028552.3	NT	Mesocricetus auratus oxiductin precursor (OVi) gene, complete cds
7074 18846			0.67	1.7E-01	ZB2910.1	NT	Human sapiens HFE gene
7272 18800	32857	2.83	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Seta-1 VT2 prophage inserted region	
7339 18868	32730	8.92	1.7E-01	BE734179.1	EST_HUMAN	601589022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'	
7494 20017	32882	1.16	1.7E-01	IP16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN ULS8 (HFLF0 PROTEIN)	
7508 24784	32883	0.73	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR	
7802 20245	33253	1.28	1.7E-01	AF000573.1	NT	Human sapiens homogentisate 1,2-dioxygenase gene, complete cds	
7804 20246	33352	0.54	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds	
8210 20760	33674	8.62	1.7E-01	7708428	NT	Human sapiens cleavage and polyacetylation specificity factor 3, 73kD subunit (CPSPF3), mRNA	
8219 20760	33675	8.62	1.7E-01	7708428	NT	Human sapiens cleavage and polyacetylation specificity factor 3, 73kD subunit (CPSPF3), mRNA	
8831 21170	34087	0.58	1.7E-01	AW9922873.1	EST_HUMAN	RC2-BN0032-1/20/2001-01-01 BN0032 Homo sapiens cDNA	
8862 21201	34119	3.28	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene	
8778 21317	34239	0.68	1.7E-01	AF217413.1	NT	Human sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced	
8778 21317	34240	0.68	1.7E-01	AF217413.1	NT	Human sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced	
9095 21631	34569	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'	
9095 21631	34570	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'	
8609 22009	34867	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14	
8614 22114	35077	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 IMAGE resequences, MAGO_Homo_sapiens cDNA	
8614 22114	35078	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 IMAGE resequences, MAGO_Homo_sapiens cDNA	
8831 22131	35088	2.47	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3	
9704 22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)	
9704 22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)	

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9722	22220	36195	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-8), (sp8 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22787	35777	0.89	1.7E-01		11427263	NT
10285	22789	35779	1.72	1.7E-01	AAB27972.1	EST_HUMAN	IMAGE:1143282 3' similar to gtl25081 TRANSFORMING PROTEIN RHOC (HUMAN)
10560	23096	36190	9.23	1.7E-01	BE390835.1	EST_HUMAN	601288547F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3813258 5'
10685	23215	36227	2.63	1.7E-01	AA814617.1	EST_HUMAN	df43e03.s1 NCI CGAP CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
10891	23505	36536	8.7	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
10891	23505	36537	8.7	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11558	24008		2.18	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
11643	24004		1.45	1.7E-01	AJ272584.1	NT	Bilobella aurantacea mitochondrial partial COII gene for cytochrome c oxidase subunit II
11847	24073	37143	4.09	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
11782	25004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	YW62x12.r1 Soares, placenta, 8 to 9 weeks, 2NbHP8tg9W Homo sapiens cDNA clone IMAGE:2587425'
12381	24549	30095	12.95	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
12839	24683		1.33	1.7E-01	AJ32510.1	NT	Sus scrofa c-fos gene, exons 1-4
131	12798	25265	1.57	1.6E-01	AF217532.1	NT	Homo sapiens melanotene kinase gene, exon 6 and 7
708	15388	25816	1.53	1.6E-01	R31497.1	EST_HUMAN	YH75f12.r1 Soares, placenta Nb21-IP Homo sapiens cDNA clone IMAGE:1355599 5'
15589	14161	28682	4.35	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1868	14552	27108	2.8	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2028	14610		1.08	1.6E-01	U10334.1	NT	Craspedolepta gigas RNA polymerase II largest subunit mRNA, partial cds
2427	15463	27559	0.98	1.6E-01	X941232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2533	15089	27072	1.12	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28008	11.95	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2917	15534	28007	11.95	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	15657	28137	1.17	1.6E-01	AE001862.1	NT	Deltapodus radiatus R1 section 1 of 2 of the complete chromosome 2
3685	16283	28735	1.35	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3685	16203	28736	1.35	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3840	16439	28901	0.71	1.6E-01	AE000982.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4072	16668		2.65	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4422	17007	28450	11.02	1.6E-01	AF178680.1	NT	Homo sapiens apelin gene, complete cds
4554	17137		3.42	1.6E-01	AW886801.1	EST_HUMAN	EST380877 MAGE sequences, MAGU Homo sapiens cDNA

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4883	17146		4.68	1.6E-01	6753310 NT		Mus musculus chaperonin subunit 3 (gamma) [Ccl3], mRNA
5057	17830	30074	0.84	1.6E-01	P40831		MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5080	17853	30093	1.45	1.6E-01	AA088343.1	EST_HUMAN	2B4H09_s1 Stratagene cDNA (#007204) Homo sapiens cDNA clone IMAGE:511381 3' similar to TR-E221955
5101	17873	30112	1.28	1.6E-01	AJ008358.1	NT	Lycoperdon esculentum RsaI fragment 2, satellite region
5101	17873	30113	1.28	1.6E-01	AJ008358.1	NT	Lycoperdon esculentum RsaI fragment 2, satellite region
5358	17918		1.81	1.6E-01	BF208302.1	EST_HUMAN	60187223F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:40366855 5'
5359	17919	30333	1.23	1.6E-01	AI874074.1	EST_HUMAN	Wm4838.X1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2439182 3'
5587	18218	30868	0.78	1.6E-01	LA06838.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30844	2.76	1.6E-01	AW197498.1	EST_HUMAN	Xm43R1_X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2886898 3' similar to TR-O75884 O75884
5713	18339	30845	2.76	1.6E-01	AW197498.1	EST_HUMAN	Xm43R01_X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2886898 3' similar to TR-O75884 O75884
5725	18351	31054	2.12	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.8 KD PROTEIN ; Ratius nonnegeicus CCAT/enhancer binding protein epsilon (cebpepsilon) gene, complete cds
6178	18789	31558	0.84	1.6E-01	BE92803.1	EST_HUMAN	RC3-BN-0034-310800-113-h01 BN0034 Homo sapiens cDNA
68559	19157	31953	2	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
68559	19157	31954	2	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7043	18083	30453	3.49	1.6E-01	AW281215.1	EST_HUMAN	UI-H-812-agl-b-08-0-1U_s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7753	20261	33157	1.44	1.6E-01	AW246359.1	EST_HUMAN	2B22248_Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7770	20278		0.75	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE:1 Homo sapiens cDNA clone PLACE:100468 5'
7810	20353	33262	1.43	1.6E-01	LA48349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7888	20510		0.55	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1(E060) /Pediatric pre-B cell acute lymphoblastic leukemia Baylor+HGS project=TCBA Homo sapiens cDNA clone TCBAPO807
8062	20604	33515	0.78	1.6E-01	U3823.1	NT	Bacteroides vulgatus beta-lactamase (cbla) gene, complete cds and mobilization protein (moba) gene, complete cds
8567	21106	34025	0.77	1.6E-01	Z89110.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2B97771 to 3213410
8760	21299	34220	0.65	1.6E-01	R13073.1	EST_HUMAN	yf80h08.17 Scarcos infant brain 1NIB Homo sapiens cDNA clone IMAGE:26873 5'
8863	21402		0.64	1.6E-01	L368861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8901	21439	34382	1.91	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
8939	21576		0.8	1.6E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds; and unknown gene
9569	22069		1.83	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041189-011-h01 ST0200 Homo sapiens cDNA
9572	22072	35033	1.86	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w

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8807	22107			1.06	1.6E-01 BE155684.1	EST_HUMAN	PM2-HT0353-270100-004-f111 HT0353 Homo sapiens cDNA
10536	23073	36087		2.7	1.6E-01 AW850853.1	EST_HUMAN	L3-CT0220-111189-028-G01 C10220 Homo sapiens cDNA
10580	23401	36418		1.55	1.6E-01 BE258849.1	EST_HUMAN	601145769F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
10584	23508			8.03	1.6E-01 AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11289	23741	36798		10.88	1.6E-01	8871552 NT	Mus musculus adipotin-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11680	25019			1.72	1.6E-01	8879468 NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkq2), mRNA
11784	24168	38776		5.34	1.6E-01 AV718695.1	EST_HUMAN	AV718695 GLC Homo sapiens cDNA clone GLCEMF07 5'
12085	24382	39988		1.55	1.6E-01 L148933.1	NT	Rat carboxylate PC5 mRNA, 5' end
12128	24382			1.75	1.6E-01 AW839711.1	EST_HUMAN	RC1-LT074-120200-014-M01 1 LT074 Homo sapiens cDNA
12229	24821			11.74	1.6E-01 AB045310.1	NT	Cucumis sativus KS mRNA for alpha-Laurene synthase, complete cds
12407	24584			5.11	1.6E-01 AK024498.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12487	24625			3.96	1.6E-01 AF287344.1	NT	Fuchsia hybrid cultivar Qiu 84208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12521	24637	30886		1.85	1.6E-01	95068522 NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Csgag5), mRNA
238	12826	25412		1.76	1.5E-01 BE71087.1	EST_HUMAN	L3-HT0818-040700-197-E05 HT0818 Homo sapiens cDNA
239	12826	25413		1.76	1.5E-01 BE71087.1	EST_HUMAN	L3-HT0818-040700-197-E05 HT0819 Homo sapiens cDNA
613	15387			2.16	1.5E-01 AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH08 5'
815	13433	25638		1.04	1.5E-01 AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C0084
-1131	13734	26244		0.84	1.5E-01 AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1138	13739	26248		2.28	1.5E-01 AJ251895.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1152	13765			1.61	1.5E-01 L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (Slc14) gene, 5' end
1258	13855	28371		0.79	1.5E-01 AW185516.1	EST_HUMAN	xn38ch11_x1 NCI CGAP_Kir11 Homo sapiens cDNA clone IMAGE:28868085 3'
1318	13912	28432		3.12	1.5E-01 D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-16)
1318	13912	28433		3.12	1.5E-01 D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1529	14121	28690		1.84	1.5E-01 AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mkk1) mRNA, complete cds
1851	14535	27091		1.62	1.5E-01 AW444451.1	EST_HUMAN	UH-BI3-akb-b-09-0-U1_s1 NCI CGAP_S1 Homo sapiens cDNA clone IMAGE:4247537 5'
2738	16281	27859		1.17	1.5E-01 BF689381.1	EST_HUMAN	xw56ac022 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gbx55072_m1
2838	15554			1.01	1.5E-01 AW572516.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3070	15885	28157		0.62	1.5E-01 M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3395	16003	28484		6.87	1.5E-01 AA835046.1	EST_HUMAN	cc68d05_s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gbx55072_m1
3415	16023	28504		0.65	1.5E-01 Z223104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3415	16023	28505		0.65	1.5E-01 Z223104.1	NT	L stagnalis mRNA for G protein-coupled receptor
							L stagnalis mRNA for G protein-coupled receptor

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							hh2802x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2858639 3' similar to contains element MER16 repetitive element :
3474	18080	28553	0.99	1.5E-01	AW612237.1	EST_HUMAN	
3819	18419	28881	2.13	1.5E-01	U08604.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3835	18434	28896	0.94	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3849	18447	28903	0.58	1.5E-01	M87882.1	NT	XNA; Thermoanaerobacterium; xnaA; 4182 base-pairs
3854	18532	28909	2.74	1.5E-01	AW685883.1	EST_HUMAN	ht0062x1 Sceas, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3851	18549	29017	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3851	18549	29018	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
4124	19717	29173	0.82	1.5E-01	AW368659.1	EST_HUMAN	RC2-HT1049-1910898-012-009 HT0148 Homo sapiens cDNA
4282	18848	29296	0.62	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C2084
4833	17411	28884	1.29	1.5E-01	BF887085.1	EST_HUMAN	602067182F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4068223 5'
4863	15221	27858	2.03	1.5E-01	BF8853289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247597 5	EST_HUMAN	6020593289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247597 5
4906	17481	28938	0.92	1.5E-01	BE173798.1	EST_HUMAN	CMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4906	17481	28939	0.92	1.5E-01	BE173798.1	EST_HUMAN	CMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL161580.2	NT	Anabiosis thaliana DNA chromosome 4, contig fragment No. 60
5461	18098	30414	1.98	1.5E-01	P07986	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF256852.1	NT	Caiman crocodilus: NHC class II beta chain (helicita) gene, complete cds
5531	18163		5.6	1.5E-01	P15198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ASBP)
5729	18355	31059	4.68	1.5E-01	AW850784.1	EST_HUMAN	IL3-CT0218-160200-084-F10 CT0218 Homo sapiens cDNA
5767	18383	31106	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5767	18383	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
6156	18768	31532	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6156	18768	31533	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6194	18804	31573	1.98	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6342	18848	31725	3.23	1.5E-01	BE727658.1	EST_HUMAN	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6394	18897		1.86	1.5E-01	4508398	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6484	19085	31887	1.76	1.5E-01	AF134907.1	NT	Influenza B virus (B/Manchurian/480984) NB protein gene, complete cds; and neuraminidase gene, partial cds
6928	24765	32027	1.94	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6952	18248	32050	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)	
6683	192389	32083	1.5	1.E-01	P48508	SWISSPROT	AMELOGENIN	
6702	19297	32101	2.16	1.E-01	Q28462	SWISSPROT	mw30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'	
6798	18377	32192	0.95	1.E-01	AA714780.1	EST_HUMAN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)	
6813	19404	32220	1.59	1.E-01	P30143	SWISSPROT		
7055	18074	30484	6.39	1.E-01	AW070295.1	EST_HUMAN	EST382376 MAGE: resequences, MAGK Homo sapiens cDNA	
7298	19798		1.9	1.E-01	AF210842.1	NT	Hom sapiens HARP (HARP) gene, exon 17 and complete cds	
7423	18947	32813	1.5	1.E-01	A1973157.1	EST_HUMAN	wf52c08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2491310 3'	
75689	20104	32979	1.02	1.E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	
75689	20104	32980	1.02	1.E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	
7590	20110	32984	1.71	1.E-01	AW500811.1	EST_HUMAN	U1-HF-BND-akk-d-05-D-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'	
7598	20110	32985	1.71	1.E-01	AW500811.1	EST_HUMAN	U1-HF-BND-akk-d-05-D-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'	
7722	20230	33119	0.71	1.E-01	U48560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los-1 (SOL3) gene, complete cds	
8002	20544	33446	1.1	1.E-01	P21303	SWISSPROT	MEROZOTE RECEPTOR PK68 PRECURSOR (88 KD PROTECTIVE MINOR SURFACE ANTIGEN) INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);	
8161	20702	33817	0.95	1.E-01	AA970317.1	EST_HUMAN	0085g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to g0:M26062	
8254	20795		1.11	1.E-01	BE884788.1	EST_HUMAN	601510523r1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'	
83338	20880		11.5	1.E-01	C168900.1	EST_HUMAN	C16800 Clontech human sorta polya+ mRNA (#8572) Homo sapiens cDNA clone GEN4-5224109 5'	
8372	20912	33832	1.82	1.E-01	L27835.1	NT	Pangasianodon gigas growth hormone (GH) mRNA, complete cds	
8520	21088	33887	2.04	1.E-01	D84478.1	NT	Human sapiens mRNA for ASK1, complete cds	
8550	21089		0.86	1.E-01	P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR	
8772	21311	34224	1.23	1.E-01	4501072	NT	Human sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA	
9033	21570	34498	2.40	1.E-01	N74226.1	EST_HUMAN	ZB68e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone NT2RP3000080 5'	
9121	21657	34568	1.06	1.E-01	BF585485.1	EST_HUMAN	PIR-S44443 S44443 RAD23 protein homolog2 - human ;	
9128	21663		2.63	1.E-01	AV754810.1	EST_HUMAN	AV754810 TP Homo sapiens cDNA clone PAAHB12.5	
9320	21640		0.94	1.E-01	AU193007.1	EST_HUMAN	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'	
9374	20313	33215	7.21	1.E-01	U00455.1	NT	Actopanser transmantano vitalogenin mRNA, partial cds	
9731	22229	35208	0.48	1.E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase 5-delta - 4-delta isomerase gene, complete cds	
9835	22333	35314	8.51	1.E-01	AF007570.1	NT	Aphylla californica carboxypeptidase D mRNA, complete cds	
9835	22333	35315	8.51	1.E-01	AF007570.1	NT	Aphylla californica carboxypeptidase D mRNA, complete cds	
10104	22589	35591	2.54	1.E-01	X98892.1	NT	P.lentisculus mRNA for integrin beta subunit	
10188	22683		3.34	1.E-01	AB027758.1	NT	Mesocritetus auratus mRNA for collagen type XVI, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10210	22705	35898	2.82	1.5E-01	AI814046.1	EST_HUMAN	WA53H12_X1_NCI_CGAP_Pt22_Homo_sapiens_cDNA_clone IMAGE:24191175_3' similar to gb:M27508_BETA_GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35899	2.82	1.5E-01	AI814046.1	EST_HUMAN	WA53H12_X1_NCI_CGAP_Pt22_Homo_sapiens_cDNA_clone IMAGE:24191175_3' similar to gb:M27508_BETA_GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22783	35775	1.75	1.5E-01	U40832.1	NT	Danio rerio transcription factor Pass8 (Pass) mRNA, complete cds
10433	22627	35939	1.97	1.5E-01	AJ011684.1	NT	Cleavicaps purpurea ps1 gene
10433	22627	35994	1.97	1.5E-01	AJ011684.1	NT	Cleavicaps purpurea ps1 gene
10704	23239	36245	5.45	1.5E-01	AL463280.2	NT	Homo sapiens chromosome 21 segment HS21C280
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C280
10854	23469	36494	1.71	1.5E-01	AWB41915.1	EST_HUMAN	IL5-CN0024-030309-025-D04 Homo sapiens cDNA IMAGE:24913103'
11045	18047	32813	2.44	1.5E-01	AI973157.1	EST_HUMAN	Wt52c08_X1_NCI_CGAP_Ut1_Homo_sapiens_cDNA_clone IMAGE:24913103'
11739	24875	70.5	1.5E-01	BF700582.1	EST_HUMAN	602128753F1_NIH_MGC_58_Homo_sapiens_cDNA_clone IMAGE:42855495'	
12125	24381		1.43	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12190	24899		7.05	1.5E-01	R83077.1	EST_HUMAN	Yp876041_X1_Soares_fetal_liver_spleen_1NFLS_Homo_sapiens_cDNA_clone IMAGE:1944305'
12288	246220		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272_XB_Homo_sapiens_cDNA_clone CBDA0D04 5'
12408	24824	30794	16.12	1.5E-01	AL138074.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 1/8
12621	246899	30882	3	1.5E-01	O9ZD78	SWISSPROT	VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-II SUBUNIT (CAV1.3)
12632	247098	30885	11.33	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12875		1.48	1.4E-01	AF008983.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8SSP to TCRBV21S2A2 region
943	135556		2.71	1.4E-01	D78358.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1302	139896		1.59	1.4E-01	TB1884.1	EST_HUMAN	yc54G01_X1_Soares_fetal_liver_spleen_1NFLS_Homo_sapiens_cDNA_clone IMAGE:1120323'
1784	14374		1.35	1.4E-01	6878880	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	28921	1.39	1.4E-01	AE00170.1	EST_HUMAN	Thamnozoa maritima section 22 of 136 of the complete genome
2028	14611		10.08	1.4E-01	AA720815.1	EST_HUMAN	ny72007_X1_NCI_CGAP_GCB1_Homo_sapiens_cDNA_clone IMAGE:12838213'
2614	15078	27850	1.4	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE PRECURSOR (GPAT)
2818	15370	27840	4.1	1.4E-01	AI833498.1	EST_HUMAN	wm74d01_X1_NCI_CGAP_U2_Homo_sapiens_cDNA_clone IMAGE:24418653'
4253	16841	28290	10.32	1.4E-01	AI886094.1	EST_HUMAN	bs56c02_X1_NCI_CGAP_L124_Homo_sapiens_cDNA_clone IMAGE:22735703'
4253	16841	28291	10.32	1.4E-01	AI886094.1	EST_HUMAN	bs56c02_X1_NCI_CGAP_L124_Homo_sapiens_cDNA_clone IMAGE:22735703'
4321	168907	28349	3.71	1.4E-01	AE00170.1	NT	Thamnozoa maritima section 22 of 136 of the complete genome
4501	170855		0.61	1.4E-01	AA776287.1	EST_HUMAN	2450b01_X1_Soares_fetal_liver_spleen_1NFLS_S1_Homo_sapiens_cDNA_clone IMAGE:4535073 3' similar to gb:201057_ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Ali repetitive element,
4784	17384	28815	0.59	1.4E-01	54539861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (Drosophila)-homolog phosphodiesterase E2 (PDE-4A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5329	17890			1.74	1.4E-01 BE810013.1	EST_HUMAN	601498056F1 NIH_MGIC_70 Homo sapiens cDNA clone IMAGE:38000167 5'	
5509	18142	30554	4.40	1.4E-01 T80877.1	EST_HUMAN	Yel15c11.51 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'		
5532	18164	30577	4.24	1.4E-01 AB004590.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds		
5532	18164	30578	4.24	1.4E-01 AB004590.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds		
6440	19042	31830	2.7	1.4E-01 BE328891.1	EST_HUMAN	hr876022.1 NCI_CGAP_Kid11 Homo sapiens cDNA clone HEMBA10007689 5'		
6508	19205	32012	8.4	1.4E-01 AU117147.1	EST_HUMAN	AU117147 HEMBA11 Homo sapiens cDNA clone HEMBA10007689 5'		
6508	19205	32013	6.4	1.4E-01 AU117147.1	EST_HUMAN	AU117147 HEMBA11 Homo sapiens cDNA clone HEMBA10007689 5'		
6586	19282	32085	3.78	1.4E-01 AW082798.1	EST_HUMAN	kb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'		
6586	19295		1.53	1.4E-01 BE368538.1	EST_HUMAN	601193532F1 NIH_MGIC_7 Homo sapiens cDNA clone IMAGE:3537581 5'		
6718	19312	32115	2.07	1.4E-01 BF378533.1	EST_HUMAN	QV1-JM0936-08036001-103-d09 UM0036 Homo sapiens cDNA		
7180	19712		0.81	1.4E-01 AL118598.1	EST_HUMAN	DKFZp761A0810_11781 (synonym: hnmr2) Homo sapiens cDNA clone IMAGE:2710289 3'		
7419	18943		1.83	1.4E-01 AW015373.1	EST_HUMAN	UH-B1D-eat-c-09-0-LII/s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'		
7617	20130	33005	1.94	1.4E-01 U85845.1	NT	Oryctodileus curicus fructose 1,6-bisphosphate adducase (AKB) gene, complete cds		
7733	20241	33132	1.77	1.4E-01 AI305192.1	EST_HUMAN	q180b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878583 3'		
8410	20850		1.28	1.4E-01 AV658047.1	EST_HUMAN	AV658047 GLC Human sapiens cDNA clone GLCFSH08 3'		
						hr82b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to TR-O02710 O02710 GAG POLYPROTEIN. ;		
8719	21258		0.62	1.4E-01 AI438683.1	EST_HUMAN			
8844	21383	34308	4.58	1.4E-01 AA307073.1	EST_HUMAN	EST1178182 Colon carcinoma (HCC) cell line Homo sapiens cDNA clone IMAGE:2487485 5'		
8924	21462	34319	0.62	1.4E-01 AW026366.1	EST_HUMAN	df55b03_y1 Morton Fetal Coochies Homo sapiens cDNA clone IMAGE:138873 6'		
9050	21587	34518	1.21	1.4E-01 R82746.1	EST_HUMAN	y10h0511 Soares placenta Nb2h1P Homo sapiens cDNA clone IMAGE:138873 5'		
9050	21587	34519	1.21	1.4E-01 R82746.1	EST_HUMAN	y10h0511 Soares placenta Nb2h1P Homo sapiens cDNA clone IMAGE:4124824 5'		
9114	21650	34591	8.48	1.4E-01 BF310569.1	EST_HUMAN	601895465F1 NIH_MGIC_19 Homo sapiens cDNA clone IMAGE:3571022 5' similar to contains zr94a04_x1 Soares_fetal_heart_Nb1H18W Homo sapiens cDNA clone IMAGE:4124824 5'		
9169	21716	34680	1.09	1.4E-01 W63411.1	EST_HUMAN	element KER repetitive element;		
9280	21806	34757	1.47	1.4E-01 Y10196.1	NT	Homo sapiens PHEX gene		
9280	21806	34758	1.47	1.4E-01 Y10196.1	NT	Homo sapiens PHEX gene		
						Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1 (ALK), and zinc finger protein (DNZ1) genes, complete cds		
9371	20310	33213	1.96	1.4E-01 AF121361.1	NT	Macromitrium levatum small ribosomal protein 4 (rpS4) gene, chloroplast gene encoding chloroplast protein, partial cds		
9898	22395	35371	1.18	1.4E-01 AF022813.1	EST_HUMAN	dt22h08_y1 Morton Fetal Coochies Homo sapiens cDNA clone IMAGE:2485094 5'		
10000	22495	35484	0.51	1.4E-01 AW021908.1	EST_HUMAN	dt22h08_y1 Morton Fetal Coochies Homo sapiens cDNA clone IMAGE:2485094 5'		
10000	22495	35485	0.51	1.4E-01 AW021908.1	EST_HUMAN	dt22h08_y1 Morton Fetal Coochies Homo sapiens cDNA clone IMAGE:2485094 5'		
10157	22652	35845	0.72	1.4E-01 BF375285.1	EST_HUMAN	MR3-ST0216-211289-013-d08 S10218 Homo sapiens cDNA		
10157	22652	35848	0.72	1.4E-01 BF375285.1	EST_HUMAN	MR3-ST0216-211289-013-d08 S10218 Homo sapiens cDNA		

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10360	22854			0.73	1.4E-01 TB4283.1	EST_HUMAN	y47763.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:111385 5'
10489	22883	35991		0.7	1.4E-01 Z90117.1	NT	Bacillus subtilis complete genome [section 14 of 21] from 2588451 to 2612870
10587	23122			1.89	1.4E-01 AA811480.1	EST_HUMAN	c860d3.s1 NCI_OGAP_GC81 Homo sapiens cDNA clone IMAGE:1320384 3'
10722	23250	38285		3.2	1.4E-01 R53400.1	EST_HUMAN	y70c05.1 Scores breast 2NIBHBS1 Homo sapiens cDNA clone IMAGE:164088 5'
10874	23489	38619		1.58	1.4E-01 P08948	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT)(INTEGRIN ALPHA-F) (MA-5) (CD49E)
11172	23879	38724		1.82	1.4E-01 X68092.1	NT	C.elegans ORF for putative membrane transport protein
11210	18943			1.98	1.4E-01 AW015373.1	EST_HUMAN	U4-H-B10-aa-c-09-0-U1.s1 NC1_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11344	23042	38052		2.4	1.4E-01 U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
12061	24344	30963		4.44	1.4E-01 X74773.1	NT	P.saita plastid gene secY
12074	24352			3.85	1.4E-01 11988117	NT	Rattus norvegicus desmin (Des), mRNA
12123	25082			1.52	1.4E-01 BE513802.1	EST_HUMAN	601315638F1 NIH MGC_8 Homo sapiens cDNA clone IMAGE:3834328 5'
12223	24444			9.33	1.4E-01 AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140W homolog, and glycineamide ribonucleotide transformylase (GART) genes, complete cds
12235	24451			1.98	1.4E-01 D84004.1	NT	Synecchocystis sp. PCC6803 complete genome, 23/27, 2868767-3002985
12315	25098			1.77	1.4E-01 P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12340	24522			2.01	1.4E-01 AA452305.1	EST_HUMAN	2c30a12.1 Scores _total_status_Nib2HF8_9W Homo sapiens cDNA clone IMAGE:7880145 similar to contains Ali repetitive element:
12345	24890			3.55	1.4E-01 D82883.1	NT	Mus musculus mRNA for prolinease, complete cds
12827	24705			1.33	1.4E-01 AW377988.1	EST_HUMAN	MRO-HT0208-221286-204-c08 HT0208 Homo sapiens cDNA
344	12898	25481		2.28	1.3E-01 4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR150) mRNA
344	12898	25482		2.28	1.3E-01 4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR150) mRNA
555	13188	25684		3.25	1.3E-01 AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
684	13288	25768		3.03	1.3E-01 AJ277608.1	NT	Human calicivirus HUNLV/Girlington/g3/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/g3/UK
684	13288	25770		3.03	1.3E-01 AJ277608.1	NT	Human calicivirus HUNLV/Girlington/g3/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/g3/UK
877	13491	26009		0.78	1.3E-01 X63320.1	NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
927	13540	26058		1.44	1.3E-01 AF138518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1064	13689	28179		1.36	1.3E-01 AL117078.1	NT	Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1168	13768			2.03	1.3E-01 AL115285.1	NT	Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370		1.36	1.3E-01 AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF-F05 5'
1463	14085			0.97	1.3E-01 AF146277.1	NT	Homo sapiens adapter protein CHAS mRNA, complete cds

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Table 4
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Probe SEQ ID NO:	Exon ORF SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mast Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14594	27143	2.32	1.3E-01	AL117078.1	NT	Bordetella diphtheriae strain T4 cDNA library under conditions of nitrogen deprivation
2215	14170		1.21	1.3E-01	AJ243578.1	NT	Rhodopsseudomonas acidophila pucB5, pucA5, pucA8, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2229	14690		1.58	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2421	14689		3.74	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
26222	15184	27750	1.55	1.3E-01	MR6818.1	NT	Cerassodus aureatus keratin type I mRNA, complete cds
3402	18011	28490	0.61	1.3E-01	AF1885779.1	NT	Homo sapiens transcription factor IgHm enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -2
3498	18103	28578	0.99	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrodipoyl transacylase mRNA, complete cds
3785	18285	28850	1.19	1.3E-01	AP0000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-281000 nt position (1/7)
3785	18385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-281000 nt position (1/7)
3791	18381	28856	0.8	1.3E-01	AB0312159.1	NT	Homo sapiens DDX4 gene for dihydrolidocid dehydrogenase 4 [AKR/TC4] exon 2
3848	18285	28850	0.62	1.3E-01	AP0000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-281000 nt position (1/7)
3848	18385	28851	0.62	1.3E-01	AP0000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-281000 nt position (1/7)
3975	18473	28837	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibroinogen, gamma polypeptide (Fn9), mRNA
4080	18857		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4125	13288	25769	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gattington/B3/UK RNA for capsid protein (ORF2), strain HUNLV/Gattington/B3/UK
4125	13288	25770	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gattington/B3/UK RNA for capsid protein (ORF2), strain HUNLV/Gattington/B3/UK
4218	16805		0.95	1.3E-01	AF020713.1	NT	Baculophage SP8c2 complete genome
4238	16826		4.04	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-038-a03 DT0018 Homo sapiens cDNA
4246	16834	28295	2.25	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate adductase mRNA, complete cds
4265	16851	28299	21.7	1.3E-01	AW273741.1	EST_HUMAN	x22f10.2x_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-28138825 3'
4404	16889		1.93	1.3E-01	AL163260.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	29693	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrodipoyl transacylase mRNA, complete cds
4631	17214	28835	2.35	1.3E-01	BE272339.1	EST_HUMAN	60112800GF1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE-28800063 5'
4898	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE-3911087 5'
5053	17629	30073	1.05	1.3E-01	D78842.1	EST_HUMAN	HUM520C02B Human placenta polyA+ (TFujikawa) Homo sapiens cDNA clone GEN-520C02 5'
5279	17841	30288	4.06	1.3E-01	AI432531.1	EST_HUMAN	HS8c10.2x_NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE-2120562 3'
5398	17854	30365	0.65	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1168000 nt position (5/7)

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5444	17989	30402	13.66	1.3E-01	AA981841.1	EST_HUMAN	045607_s1 Scores_basis_NIH Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YE56_YEAST P40093 HYPOTHETICAL_38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17989	30403	13.68	1.3E-01	AA981841.1	EST_HUMAN	045607_s1 Scores_basis_NIH Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YE56_YEAST P40093 HYPOTHETICAL_38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5628	18160	30575	0.69	1.3E-01	AW468988.1	EST_HUMAN	L1 repetitive element;
5685	18198	30842	2.78	1.3E-01	AW804417.1	EST_HUMAN	QVO-UH00583-10040-189-a08 UMM083 Homo sapiens cDNA
56892	18318		0.78	1.3E-01	AF107783.1	NT	Emenecilla nidulans DNA-dependent RNA polymerase II RPB2/40 (RPB2) gene, partial cds
5772	18387		0.76	1.3E-01	AF058880.1	NT	Hepatitis C virus 88_Cl10 genome polyprotein-gene, partial cds
5889	18521	31248	0.80	1.3E-01	BF210920.1	EST_HUMAN	601874891F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6809	18208	32014	15.81	1.3E-01	AB031328.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6884	18250	32083	2.07	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (rod allele)
6883	19618		0.82	1.3E-01	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.84	1.3E-01	H48864.1	EST_HUMAN	yf340021r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
7800	20442		0.67	1.3E-01	BE272359.1	EST_HUMAN	601128086F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:29890083 6'
7814	20456	.33382	1.62	1.3E-01	11423284	NT	Human sepiants PRO00611 protein (PRO00611), mRNA
7845	20487	33397	0.89	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8180	20721		0.47	1.3E-01	BE562528.1	EST_HUMAN	601335628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8286	20927		4.61	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8325	20988		3.78	1.3E-01	88232910	NT	Homo sapiens core histone macroH2A.2 (MACROH2A2), mRNA
8465	21005	33923	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8878	21418	34339	0.52	1.3E-01	R11172.1	EST_HUMAN	yf39g11_r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN :
8878	21418	34340	0.52	1.3E-01	R11172.1	EST_HUMAN	SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN :
6148	21681	34625	1.84	1.3E-01	11068003	NT	Pluteus xylosteus granulosus, complete genome
8146	21681	34626	1.84	1.3E-01	11068003	NT	Pluteus xylosteus granulosus, complete genome
83893	21816	34768	5.08	1.3E-01	AF023129.1	NT	Oncotilus cinctulus H ⁺ -ATPase alpha 2c subunit mRNA, complete cds
8888	22185		0.8	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
8884	22458		0.8	1.3E-01	8339040	NT	Rattus norvegicus peptidyl arginine diaminopeptidase, type IV (Pd4), mRNA
10036	22531	35520	0.83	1.3E-01	AW851589.1	EST_HUMAN	MR2-CT0222-201089-001-a01 CT0222 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
102822	247977	35776	0.9	1.3E-01	AL168246.2	NT	Homo sapiens chromosome 21 segment HS21C046
104117	22911	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone IMAGE:1002387 5'
105111	23049		3.33	1.3E-01	BF320699.1	EST_HUMAN	MR4-BT0358-130700-010-H08_B10358 Homo sapiens cDNA
108715	23400	36520	1.58	1.3E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11130	23638		5.19	1.3E-01	6871745	NT	Mus musculus coflin 2, muscle (Cf2), mRNA
11488	23918	36984	3.61	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11802	24241	31007	1.64	1.3E-01	BE818346.1	EST_HUMAN	6014627741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38868003 6'
12048	24332		3.27	1.3E-01	AJ242780.1	NT	Celius galutus sox1 gene for lymphobactin, exons 1-3
12488	24594		1.63	1.3E-01	AW001114.1	EST_HUMAN	W24409_1X1 Soares_Diethylstilbestrol_cDNA clone IMAGE:2520977 3' similar to gb:U05780_mer1
12847	24721		1.84	1.3E-01	BE958803.1	EST_HUMAN	TR-080287_O80287 KIAA0539 PROTEIN_;
408	13061	25573	10.61	1.2E-01	AI421744.1	EST_HUMAN	601844622P2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928880 3'
449	12678		1.43	1.2E-01	U68912.1	NT	Dicystostelium discoideum ORF DG1016 gene, partial cds
573	13203		2.58	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1419	14012	26541	2.31	1.2E-01	AI149148.1	EST_HUMAN	AU149148 NT2RMA0011691 3'
1419	14012	26542	2.31	1.2E-01	AI149148.1	EST_HUMAN	AU149148 NT2RMA0011691 3'
1428	14019		3.26	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cDNA clone cDNA_B11 5'
1431	14023		6.68	1.2E-01	AL45068.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1554	14148		1.19	1.2E-01	AA89747.1	EST_HUMAN	el48cc09_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:14605684 3' similar to TRQ18871
1673	14265	28799	1.48	1.2E-01	Q14934	SWISSPROT	Q16871 ANTRI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR_;
1691	14283	28819	2.77	1.2E-01	AI285402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NFAT3)
1805	14395		21.02	1.2E-01	X08921.1	NT	H.sapiens DNA for endogenous retroviral like element
1864	14548		2.23	1.2E-01	AW443268.1	EST_HUMAN	U1-H813-ab-e-10-0-U1-s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2228	14801	27373	1.31	1.2E-01	BF248480.1	EST_HUMAN	601821687F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4048224 6'
2325	14886	27470	1.08	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2418	14984		1.05	1.2E-01	Z24405.1	EST_HUMAN	HSAAAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA
2625	15167	27754	1.38	1.2E-01	AW988556.1	EST_HUMAN	QV3-BN0046-2203601-128-f10 BN0046 Homo sapiens cDNA clone IMAGE:22288988 3' similar to TRQ14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element;
2754	15309	27875	1.11	1.2E-01	AH223888.1	EST_HUMAN	hs1Bq07_1X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:22288988 3' similar to TRQ14048 Q14048
2868	15486	27898	1.22	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
28277	15543	28019	2.37	1.2E-01	AI720470.1	EST_HUMAN	as80-08x1 Bertrand cation HPLB7_Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb105085
28811	15577	28056	3.29	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN); Human creatine kinase-B mRNA, complete cds
30337	15653	28132	0.83	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
32867	15876	28382	2.08	1.2E-01	AW370988.1	EST_HUMAN	QV1-8710259-261089-021-d05 B101259 Homo sapiens cDNA
32868	15897		1.19	1.2E-01	U6780.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
35225	16130		0.62	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
35733	16177	28659	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
35733	16177	28680	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
36886	16130		1.09	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
38333	18432		0.84	1.2E-01	BF128551.1	EST_HUMAN	001610788r1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053868 3'
42621	18847	29294	1.88	1.2E-01	Z6425.1	NT	P.clavata mRNA; repeat region (D 24IR77)
42621	18847	29295	1.88	1.2E-01	Z6425.1	NT	P.clavata mRNA; repeat region (D 24IR77)
44022	16897	28431	0.6	1.2E-01	M15881.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
48320	17408	28862	0.98	1.2E-01	Z48183.1	NT	L.esculentum mRNA for glycosidase-1
48909	17484		2.83	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
61633	17732	30159	1.08	1.2E-01	BF577357.1	EST_HUMAN	6021351185r1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4280165 5'
52275	17838	30262	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
52275	17838	30263	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
54223	17880		1.89	1.2E-01	AL1627757.2	NT	Neisseria meningitidis serogroup A strain Z2461 complete genome; segment 6/7
54571	18092	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	ny6304.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282650 3'
55033	18137	30547	1.13	1.2E-01	AF223381.1	NT	Homo sapiens calcium channel alpha1E subunit(CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
55113	18148	30557	2.28	1.2E-01	W33035.1	EST_HUMAN	z008002.r1 Soares_parenthroid_tumor_Nb-HPA_Homo sapiens cDNA clone IMAGE:321689 5'
55711	18202	30652	2.3	1.2E-01	Z89286.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
56986	18322	30822	0.89	1.2E-01	Z48234.1	NT	M.domestica Barth, Grammy Smith edit mRNA for alcohol dehydrogenase
63447	18862	31731	1.81	1.2E-01	BE620945.1	EST_HUMAN	601463518r1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885613 5'
63395	18898	31777	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
64411	18943	31831	2.38	1.2E-01	AW845275.1	EST_HUMAN	IL0-C031-221088-113-604 CT0031 Homo sapiens cDNA
65022	19102	31887	1.59	1.2E-01	M26925.1	NT	Mouse galactosidase transferase mRNA, complete cds
67755	18348	32157	0.88	1.2E-01	BF347885.1	EST_HUMAN	602023112F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156388 5'
78333	20375		1.31	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-f09 BN0137 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7903	20445	33351	3.58	1.2E-01	AI913753.1	EST_HUMAN	wc8903.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW.GST2_HUMAN	
7950	20482	33401	0.72	1.2E-01	Q02369	SWISSPROT	Q89755 MICROSONAL GLUTATHIONE S-TRANSFERASE II; NADH+UBIQUINONE OXIDOREDUCTASE B2 SUBUNIT (COMPLEX I-B22) (CH-B22)	
8251	20732	33709	0.9	1.2E-01	AI832681.1	EST_HUMAN	ef71b10.x1 Barstiedt clone HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'	
8335	20878		0.03	1.2E-01	AW083852.1	EST_HUMAN	xc19d07.x1 NCI_CGAP_Eco2 Homo sapiens cDNA clone IMAGE:2587587 3' similar to gb:NM13452 LAMINA (HUMAN);	
8355	20895			4.17	1.2E-01	AF053772.1	NT	
8392	20932	33852	0.82	1.2E-01	J03956.1	NT	N.crasse vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds	
8392	20932	33853	0.82	1.2E-01	J03956.1	NT	N.crasse vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds	
8537	21076			0.83	1.2E-01	AJ271738.1	NT	
8823	21182			2.14	1.2E-01	U32714.1	NT	
8857	21198			0.85	1.2E-01	X15191.1	NT	
9491	21947			2.86	1.2E-01	X77081.1	NT	
8918	22414	35398	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Ccl Homo sapiens cDNA clone CUAKE08 5'	
10155	22650	35644	0.48	1.2E-01	AI718395.1	EST_HUMAN	es56p09.x1 Barstiedt clone HPLRB7 Homo sapiens cDNA clone IMAGE:23330566 3'	
10788	23260		3.58	1.2E-01	D26184.1	NT	Yeast MFT5 gene for suppressor protein, complete cds	
10944	23400			3.87	1.2E-01	BE982324.2	EST_HUMAN	6016555778R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
11026	23540			1.62	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11134	23842	36882	2.67	1.2E-01	AF190463.1	NT	Human sapiens dynamin intermediate chain DNA11 (DNA11) gene, exon 17	
11183	23868	36748	1.67	1.2E-01	R40249.1	EST_HUMAN	yf60c02.81 Soares infant brain T11B Homo sapiens cDNA clone IMAGE:288890 3'	
11382	23834			1.8	1.2E-01	M65108.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11687	24090			4.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12028	24319			4.43	1.2E-01	AJ271738.1	NT	Human sapiens Xq pseudautosomal region; segment 2/2
12109	25038	30503	3.9	1.2E-01	Q048112	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN PRECURSOR (MSP RECEPTOR) (P1B5-RON) (CDW 138) (CD138 ANTIGEN)	
12228	24447			1.95	1.2E-01	AF188982.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaenin gene, partial cds
12220	13203			17.94	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds .
12345	24526			1.81	1.2E-01	X53981.1	NT	R.Jonzeicus NF68 gene for f68kDa neurofilament
12440	24577	30815	8.5	1.2E-01	AI288603.1	EST_HUMAN	gi20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:18588840 3'	
12463	24591			2.19	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12468	24972			9.71	1.2E-01	O98433	SWISSPROT	CYCLIN T

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Probe SEQ ID NO:	Event SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12849 16130			1.65	1.2E-01 Z99118.1	NT		<i>Escherichia coli</i> complete genome (section 15 of 21); from 2785131 to 3013540
580 13220	25896		0.8	1.1E-01 AF561003.1	EST_HUMAN	nt 8d08_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167883 3'	
643 13268	25743		2.98	1.1E-01 AA568006.1	EST_HUMAN	nm08g11.51 NCI_CGAP_Cat0 Homo sapiens cDNA clone IMAGE:1059820 3' similar to gp>08885_m1	
1082 13697	28207		1.54	1.1E-01 BF897308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN); 60212847/F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286771 5'	
1124 13727			1.48	1.1E-01 AL161580.2	NT	Arribalzaga thaliana DNA chromosome 4, contig fragment No. 80	
1201 15435	28314		3.68	1.1E-01 AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA	
1282 13887	28411		1.89	1.1E-01 D8404.1	NT	Synechocystis sp. PC-6803 complete genome, 2/327, 2886787-3002885	
1568 14160	26691		2.94	1.1E-01 AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'	
2253 14824			3.72	1.1E-01 6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pcre), mRNA	
2576 16401			1.24	1.1E-01 6978878	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA	
2602 15164			1.08	1.1E-01 AW821908.1	EST_HUMAN	RCO-ST0379-210100-032-904 ST13379 Homo sapiens cDNA, Interneulin-12 p35 subunit [intra, Genbank, 700 nt, segment 4 of 5]	
2880 15498	27883		1.17	1.1E-01 S82418.1	NT	HSCIRP22 normalized infant brain cDNA Homo sapiens cDNA clone c-11f02 3'	
3068 16883	28155		0.78	1.1E-01 F03265.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenva1g), mRNA	
3385 15894			1.67	1.1E-01 6753221	NT	601308678/F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'	
3468 16075	28548		2.27	1.1E-01 BE383188.1	EST_HUMAN	C.reinhardtii nuclear gene on linkage group XIX	
3489 16104	28579		1.59	1.1E-01 X62135.1	NT	Y062208..1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;	
3538 16143	28628		0.59	1.1E-01 R98946.1	EST_HUMAN	Alu repetitive element;	
3842 16245	28720		0.8	1.1E-01 Y07685.1	NT	Alimarusus gene for transposase	
3783 16384			1.35	1.1E-01 P97384	SWISSPROT	ANNEXIN XI (CALYCULIN-ASSOCIATED ANNEXIN 50) (CAP-50)	
3771 16372	28837		1.61	1.1E-01 X52708.1	NT	G.gallus gene encoding non-Histone chromosome protein HMIG-14b, exons 4 and 5	
4188 16778	29223		1.61	1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-907 ST10280 Homo sapiens cDNA	
4188 16778	29224		1.61	1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-907 ST10280 Homo sapiens cDNA	
4339 16926			12.27	1.1E-01 AF157088.1	NT	Drosophila melanogaster karsicht protein (kar) mRNA, complete cds	
4374 16961	29407		0.63	1.1E-01 AW802059.1	EST_HUMAN	IL5UMD070-020500-038-908 UMG070 Homo sapiens cDNA	
4745 17328	29768		1.11	1.1E-01 S44657.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, 8 cell lymphoma line 36C13, Genomic, 1973 nt, segment 1 of 7]	
4958 17533	28975		1.21	1.1E-01 Y07695.1	NT	Alimarusus gene for transposase	
5169 16784			0.78	1.1E-01 AFC30001.1	NT	Mus musculus major histocompatibility locus class III region butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, parathyroid hormone/thyrotropin receptor complex	
5431 17988	30392		4.82	1.1E-01 AV730589.1	EST_HUMAN	AV730589 HTTF Homo sapiens cDNA clone HTFAAG12 5'	
5431 17988	30393		4.82	1.1E-01 AV730589.1	EST_HUMAN	AV730589 HTTF Homo sapiens cDNA clone HTFAAG12 5'	

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	18245	28720	0.57	1.1E-01	Y07695.1	NT	A_immersus gene for transposase nx7603_s1_NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:12681140 similar to contains Alu repetitive element
5850	18474		4.49	1.1E-01	AA747218.1	EST_HUMAN	elementcontains element MIER35 repetitive element;
5904	18536	31201	1.17	-1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	6020389176F1_NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4188818_5'
5974	18594	31329	0.84	1.1E-01	BF339519.1	EST_HUMAN	6020389176F1_NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4188818_5'
6001	18621	31356	2	1.1E-01	X68851.1	NT	S.pombe sas8 gene encoding protein kinase
6031	18830	31391	5.02	1.1E-01	M085533.1	NT	Providencia rettgeri penicillin O amidase gene
6177	18787	31555	1.75	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6197	18897	31578	1.6	1.1E-01	BE7681152.1	EST_HUMAN	PM3-FT0024-130800-004-f12_FT0024 Homo sapiens cDNA RC3-CT0254-280888-011-e01 CT0254 Homo sapiens cDNA
6216	18826	31598	7.81	1.1E-01	AW853689.1	EST_HUMAN	RC3-CT0254-280888-011-e01 CT0254 Homo sapiens cDNA clone RL43
6562	19180	31958	1.98	1.1E-01	AF035748.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6599	19198	32001	0.84	1.1E-01	AI216307.1	EST_HUMAN	97800601 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841098_3'
6721	18315	32118	3.92	1.1E-01	O88635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19398		3.07	1.1E-01	AF032922.1	NT	Homo sapiens synthase 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6888	19623	32458	2.38	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF7382758.1	EST_HUMAN	601816524F1_NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050353_5'
7345	24780	32737	0.92	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA. 1168001-1485000 nt, position (87)
7542	20082	32835	7.24	1.1E-01	BF884628.1	EST_HUMAN	602140876F1_NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019_5'
7542	20082	32836	7.24	1.1E-01	BF884628.1	EST_HUMAN	602140876F1_NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019_5'
7851	20163	33051	1.85	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7882	20183		0.7	1.1E-01	214088.1	NT	B_subtilis gene encoding hypothetical polypeptide synthase
7883	20194	33082	3.53	1.1E-01	AA788784.1	EST_HUMAN	ah31006_s1 Soares_Parathyroid_tumor_NbHPA_Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRANIN A PRECURSOR (HUMAN);
7898	20451	33358	1.41	1.1E-01	U67482.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8148	20860	33603	1.6	1.1E-01	AA483574.1	EST_HUMAN	nh04g10_s1_NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8148	20860	33604	1.6	1.1E-01	AA483574.1	EST_HUMAN	nh04g10_s1_NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8197	20738	33850	1.18	1.1E-01	X91233.1	NT	H.sapiens IL15 gene
8235	20778		1.15	1.1E-01	AW817981.1	EST_HUMAN	PM1-ST0270-080200-001-f09_ST0270 Homo sapiens cDNA
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P184_11547 (synonym: Ifnar1) Homo sapiens cDNA clone DKFZp547P184_5'
8752	21281	34211	8.48	1.1E-01	U02482.1	NT	Padicoccus acidilactici H plasmid pSMB74 lacZ production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8843	21382	34307	0.87	1.1E-01	A1807474.1	EST_HUMAN	Wf48c01_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816_3' similar to contains Alu repetitive element

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
88358	21470	34397	0.48	1.1E-01 AF050061.1	NT	Homo sapiens C1orf3 large protein mRNA, complete cds	
88773	21511	34433	2.22	1.1E-01 AA182153.1	EST_HUMAN	2P83612.1 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'	
88773	21511	34434	2.22	1.1E-01 AA182153.1	EST_HUMAN	2P83612.1 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'	
80032	21589	34528	0.82	1.1E-01 Y12727.1	NT	P_furiosus partial diph5 gene and srf5 gene	
80032	21628	34585	2.28	1.1E-01 T72875.1	EST_HUMAN	JY18HC3_51 Scores fetal liver spleen 1NFLs Homo sapiens cDNA clone IMAGE:108725 3' similar to jg18hc3_51 Scores fetal liver spleen 1NFLs Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:NM81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2(HUMAN);	
61119	21655	61119	0.67	1.1E-01 BE882280.1	EST_HUMAN	601436872F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:30222048 5'	
6343	21837	6343	1.13	1.1E-01 BE142305.1	EST_HUMAN	CM3-HT0142-271089-028-g11 HT0142 Homo sapiens cDNA MR2-CHN0227-040900-005-ad8 GB0227 Homo sapiens cDNA	
64117	21928	64117	2.2	1.1E-01 BF085149.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43	
88324	22322	88324	0.6	1.1E-01 AL161549.2	NT		
10107	22032	10107	1.03	1.1E-01 R80560.1	EST_HUMAN	JY8608_51 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:147084 3'	
10240	22735	35727	0.88	1.1E-01 U60528.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds	
10554	23080	30104	1.6	1.1E-01 AF248277.1	NT	Dichotomium discoidatum kinesin Unc104Kif1a homolog (Unc104) mRNA, complete cds	
10084	15853	20153	2.12	1.1E-01 F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'	
16802	23525	16802	3.23	1.1E-01 AF168032.1	NT	Carassius auratus activin beta A precursor mRNA, complete cds	
						YJ35112.1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131758 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;	
10823	23442	38463	3.76	1.1E-01 R237078.1	EST_HUMAN	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA	
10831	23449	38470	1.85	1.1E-01 6881351 NT		Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	
10847	18587	31298	1.56	1.1E-01 AL110985.1	NT	M.musculus Cytokine gene	
11000	23572	38009	1.74	1.1E-01 X70058.1	NT	Z.mobilis Ig and Ig genes encoding rRNA guanine transglycosylase and DNA ligase	
11085	23587	38833	3.35	1.1E-01 Z11910.1	NT	Z.mobilis Ig and Ig genes encoding rRNA guanine transglycosylase and DNA ligase	
11085	23587	38834	3.35	1.1E-01 Z11910.1	NT	Z.mobilis Ig and Ig genes encoding rRNA guanine transglycosylase and DNA ligase	
11188	23891	38738	2.89	1.1E-01 P17427	SWISSPROT	SKIN SECRETORY PROTEIN XP22 PRECURSOR (APEG PROTEIN)	
11884	24231	4.01	1.1E-01 BE707023.1	EST_HUMAN	RC2-NT0112-120600-014-03 NT0112 Homo sapiens cDNA DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)		
12143	24835	32.29	1.1E-01 BE974558.1	EST_HUMAN	6016805651R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'		
12587	24894	30880	1.89	1.1E-01 BF238753.1	EST_HUMAN	6011805350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'	
1243	13341	2.35	1.0E-01 O02855		SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)	
1315	13609	28429	1.92	1.0E-01 AB85469.1	EST_HUMAN	WS08d01_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2498577 3' similar to contains MER7.13 repetitive element;	
14326	14028	26557	2.23	1.0E-01 AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16	
2531	15095	27887	0.97	1.0E-01 AW451385.1	EST_HUMAN	UH-B13-abc-d-07-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'	
33633	16167	28849	1.04	1.0E-01 BF038981.1	EST_HUMAN	601456301F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:38569849 5'	
3782	16382	28847	0.82	1.0E-01 BF238818.1	EST_HUMAN	6011805489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'	
3904	16503	28864	1.41	1.0E-01 AF287061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes	

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3904	16503	28965	1.41	1.0E-01	AF287081.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes	
4027	16525	29097	2.82	1.0E-01	BF365703.1	EST_HUMAN	QV2-N10048-160800-316-005 NT 0048 Homo sapiens cDNA	
4498	17080	28529	1.62	1.0E-01	AE002205.2	NT	Chlamydomonas pneumoniae AR39, section 91 of 94 of the complete genome	
4653	17235		0.97	1.0E-01	AI792349.1	EST_HUMAN	an2204.y5 Gaestier Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'	
4822	17400	28853	1.8	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fcr) mRNA, complete cds	
4920	17485	28946	0.86	1.0E-01	AA785434.1	EST_HUMAN	ca05H03.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1304117 3'	
5050	17623	30068	2.12	1.0E-01	AW852344.1	EST_HUMAN	EST384414 MAGE resequences, MAGB Homo sapiens cDNA	
5408	17885	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQE10 5'	
5415	17972		0.88	1.0E-01	AV763380.1	EST_HUMAN	AV763380 MDS Homo sapiens cDNA clone IMAGE:416695 3'	
5524	18159		0.57	1.0E-01	W86490.1	EST_HUMAN	Zh62104.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'	
6040	18859		0.85	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds	
6175	18798	31554	11.01	1.0E-01	AF274975.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds	
6477	19078	31981	0.98	1.0E-01	AA481678.1	EST_HUMAN	Zn41910.s1 Soares_early tumor NbHOT Homo sapiens cDNA clone IMAGE:758258 3' similar to contains	
6489	19090	31873	0.82	1.0E-01	AA406039.1	EST_HUMAN	L1.13 L1 repetitive element;	
7081	19852		1.71	1.0E-01	R23821.1	EST_HUMAN	ZL67c12.s1 Soares_teats_NHT Homo sapiens cDNA clone IMAGE:743082 3'	
7717	20225		2.33	1.0E-01	Y12488.1	NT	Y34406.s1 Soares_placenta Nb21P Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;	
7874	20416	33324	0.53	1.0E-01	AA861091.1	EST_HUMAN	dk32g01.s1 Soares_teats_NHT Homo sapiens cDNA clone IMAGE:1407686 3' similar to gb:NM34182 CAMP. DEPENDENT PROTEIN KINASE GAMMA-CATALYTIC SUBUNIT (HUMAN);	
8107	20648		0.6	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA	
8429	20869		0.63	1.0E-01	AW189787.1	EST_HUMAN	x109b01.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2875689 3' similar to db>X17203 40S RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.k3 TAR1 repetitive element;	
9113	21649	34590	1.08	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synman mRNA, complete cds	
9418	21825	34873	0.49	1.0E-01	R44893.1	EST_HUMAN	Y033H04.s1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'	
9426	21835		2.05	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds	
9469	21868		2.67	1.0E-01	AE001501.1	NT	Halichoeretes pyrrhopygia, strain 389 section 82 of 132 of the complete genome	
9483	21940	34898	0.71	1.0E-01	W01855.1	EST_HUMAN	ZG68c10.s1 Soares_cDNA clone IMAGE:327282 3'	
9735	22233	35211	1.67	1.0E-01	BF240154.1	EST_HUMAN	801905681F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'	
9848	22346	35327	8.17	1.0E-01	AB046788.1	NT	Homo sapiens mRNA for KIAA1679 protein, partial cds	
9849	22346	35328	8.17	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds	
10048	22543		2.05	1.0E-01	AW857425.1	EST_HUMAN	EST388615 MAGE resequences, MAGB Homo sapiens cDNA	
10053	22548	35542	0.61	1.0E-01	T51952.1	EST_HUMAN	Y028a06.s1 Stratego fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element	

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Table 4
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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22728	35720	1.08	1.0E-01	BE752750.1	EST_HUMAN	601584804F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3889098 5'
10537	23074		2.11	1.0E-01	AU158127	EST_HUMAN	AU158127 THYRO1 Homo sapiens cDNA clone THYRO1000888 3'
10910	23429	38448	3.33	1.0E-01	BF242948.1	EST_HUMAN	601677703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23428	38449	3.33	1.0E-01	BF242945.1	EST_HUMAN	601677703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	38788	5.03	1.0E-01	BE780543.1	EST_HUMAN	6015845568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3889734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601086554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12104	24366		1.74	1.0E-01	7062165 NT	Homo sapiens KIAA0514 gene product (KIAA0514). mRNA	
12122	24380		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster fz gene
12338	24519		2.27	1.0E-01	AA737081.1	EST_HUMAN	mx11c08_s1 NCI_CGAP_Gc3 Homo sapiens cDNA clone IMAGE:1255780 3'
12413	25031		4.74	1.0E-01	U526891.1	NT	Corynebacter polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE537719.1	EST_HUMAN	601086554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12495	24623		1.83	1.0E-01	BE168905.1	EST_HUMAN	QV4-HT0401-211288-084-803 HT10401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24874		7.73	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
22008	15358	27825	0.83	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (p80-RII) mRNA, complete cds
28113	15385	27834	1.95	9.9E-02	BE54554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
28113	15386	27835	1.95	9.9E-02	BE54554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
33005	15816	28383	1.96	9.9E-02	AF088010.1	NT	Homo sapiens neuretin III-alpha gene, partial cds
4025	16623	28095	0.84	9.9E-02	A1821637.1	EST_HUMAN	z445c03_s5 Sodates ovary tumor NIH3T3 Homo sapiens cDNA clone IMAGE:740932 3'
7049	18088	30459	9.12	9.9E-02	D83710.1	NT	Aspergillus terreus Bsd mRNA for blastidin S deaminase, complete cds
7856	20398	33304	0.65	9.9E-02	AW103088.1	EST_HUMAN	x443c08_x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2589528 3' similar to contains Ali repetitive element; contains element MIR MIR repetitive element;
7856	20398	33305	0.65	9.9E-02	AW103088.1	EST_HUMAN	x443c08_x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2589528 3' similar to contains Ali repetitive element; contains element MIR MIR repetitive element;
9181	21758	34704	1.1	9.9E-02	8755111 NT	Mus musculus phosphatid transfer protein (Ptp), mRNA	
589	13219		1.48	9.9E-02	X56338.1	NT	O.sativa RAMy3C gene for alpha-amylase
3179	15762	28263	4.23	9.9E-02	AF184274.1	NT	Daucus carota leucanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	16894	28337	8.69	9.9E-02	AF257329.1	NT	Leptospireria maculans beta-tubulin mRNA, complete cds
4308	16894	28338	8.69	9.9E-02	AF257329.1	NT	Leptospireria maculans beta-tubulin mRNA, complete cds
7495	20018		0.99	9.9E-02	X541133.1	NT	Human HTP delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.9E-02	M61943.1	NT	Human laminin B1 chain gene, exon 28
11134	23032	36041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884287 5'
111840	24203		1.46	9.8E-02	83939751 NT	Rattus norvegicus microtubule-associated protein tau (Mapt). mRNA	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1384	13888	28516	1.24	9.7E-02	AB005308.1	NT	Abo arborans mRNA for NADP-halic enzyme, complete cds
1629	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE108960.1	EST HUMAN	QV1+HT0516-070300-085-e04 HT0516 Homo sapiens cDNA
4055	168352		4.78	9.7E-02	Q99785	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF088189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnscC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF088189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnscC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW85476.1	EST HUMAN	ES1366546 MAGE resequences, MAGC Homo sapiens cDNA
7340	19857	32731	3.26	9.7E-02	2589119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410
7824	20468	33374	1.29	9.7E-02	N22798.1	EST HUMAN	yw41cd3_s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788_3'
7824	20468	33375	1.28	9.7E-02	N22798.1	EST HUMAN	yw41cd3_s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788_3'
8783	21322	34246	1.47	9.7E-02	AI853984.1	EST HUMAN	wx78008x1 NCI CGAP_OX38 Homo sapiens cDNA clone IMAGE:2549747_3' similar to gb:X52851_m81 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11076	23593		2.34	9.7E-02	U58337.1	NT	Mus musculus Igf1n (Igf1n) mRNA, partial cds
2080	14640	27213	1.33	9.6E-02	AI080721.1	EST HUMAN	cz47411_x1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:1878485_3'
2080	14640	27214	1.33	9.6E-02	AI080721.1	EST HUMAN	cz47411_x1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:1878485_3'
4437	17023	29463	7.54	9.6E-02	232888.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
5142	17713	30144	1.03	9.6E-02	AW68230.1	EST HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
6254	18883		2.74	9.6E-02	BE91039.1	EST HUMAN	601489088f NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165_5
8317	20858		0.61	9.6E-02	AU137084.1	EST HUMAN	AU137084 PLACE:1 Homo sapiens cDNA clone PLACE:1003740_5'
9463	21988	34644	1.34	9.6E-02	AY887888.1	EST HUMAN	AY887888 GKC Homo sapiens cDNA clone GKCAAH02_5'
9788	22284		1.35	9.5E-02	BE894885.1	EST HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918333_5
9852	22447	35429	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMB11 candidate tumour suppressor gene, exons 1 to 55
9852	22447	35430	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMB11 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35544	1.28	9.6E-02	AB013985.1	NT	Antennular major transposon Tam3 pseudogene for transposase (In S-S copy)
10055	22550	35545	1.28	9.6E-02	AB013985.1	NT	Antennular major transposon Tam3 pseudogene for transposase (In S-S copy)
10158	22854	35849	3.43	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10621	23153	36185	7.28	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
11569	24013	37082	1.81	9.6E-02	AA625755.1	EST HUMAN	z181go1_s1 Soares_NHT Homo sapiens cDNA clone IMAGE:745382_3'
12486	24617		1.55	9.6E-02	H14598.1	EST HUMAN	ym181o3_s1 Soares Infant brain 11NB Homo sapiens cDNA clone IMAGE:488533_3'
4177	16768	28217	2.24	9.5E-02	AW882395.1	EST HUMAN	CM2-BN0023-050200-087-f12 BN023 Homo sapiens cDNA
5286	17848	30274	1.12	9.5E-02	U63374.1	NT	Lycopisoon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5846	18470	31190	0.82	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7344	18871	32738	4.47	9.5E-02	AB003473.1	NT	Triturus vulgaris DNA for phospholipase A2 inhibitor, complete cds
7569	20088	32863	6.95	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7885	18470	31190	0.9	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7821	20363	33271	2.04	9.5E-02	BFO059881.1	EST_HUMAN	601453842F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857243 5'
7821	20363	33272	2.04	9.5E-02	BFO059881.1	EST_HUMAN	601453842F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	38107	3.19	9.5E-02	BFO059861.1	EST_HUMAN	601453842F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	38108	3.19	9.5E-02	BFO059861.1	EST_HUMAN	601453842F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857243 5'
12557	24658		2.4	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1873	14458	27015	3.67	9.4E-02	BF071063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
1804	14480	27050	1.38	9.4E-02	U55944.1	NT	Carica porcata 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1804	14480	27051	1.38	9.4E-02	U55944.1	NT	Carica porcata 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3849	16547	28015	5.59	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5383	17542		0.83	9.4E-02	X98106.1	NT	Lactobacillus bacteriophage phi16 complete genomic DNA
6459	19080	31848	0.73	9.4E-02	AF067363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
85336	21075		2.32	9.4E-02	Z46863.1	NT	Actinobacter sp. CVD, cobQ, sodM, lytS, rnbA, rnbB, estB, oxyR, ppk, rntA, ORF2 and ORF3 genes
10813	20107	32882	2.33	9.4E-02	L78833.1	NT	Human BRCA1, Rh07 and vati genes, complete cds, and lf635 gene, partial cds
11722	24834		6.48	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12845	24719	30880	3.54	9.4E-02	U27689.1	NT	Human pephBTG-1 betaine-GABA transporter mRNA, complete cds
3018	16824		1.68	9.3E-02	4869280	NT	Human BA11-associated protein 3 (BA1AP3) mRNA
3063	15679		7.31	9.3E-02	6912525	NT	Human esopharyngeal epithelium specific protein 1 (NESG1), mRNA
32865	15906	28387	2.05	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288289 5'
4232	16820	28269	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3807653 5'
4232	16820	28270	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3807653 5'
4840	17418		1.28	9.3E-02	AV732224	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5843	18467		0.73	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8190	20731	33643	0.52	9.3E-02	AW668007.1	EST_HUMAN	EST89 Human Fetal Brain MATCHMAKER cDNA Library/Homo sapiens cDNA
9052	21589		0.5	9.3E-02	AL113178.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
9828	22126	35090	2.1	9.3E-02	BE982831.2	EST_HUMAN	601655888R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3855881 3'
10094	22589	35581	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10094	22589	35582	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10222	22717		3.82	9.3E-02	AW206117.1	EST_HUMAN	U1+BN1-afx-h-05-U1..1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:272553 3'
11692	24854		2.27	9.3E-02	AJ248850.1	NT	Photobacterium damselae subsp. damselae partial gyrfB gene for DNA gyrase B subunit

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
12379	24986		16.03	9.3E-02 AW488850.1	EST_HUMAN	hd26h12.01 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'		
12389	24933			3.18	9.3E-02 AF100856.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Blng1 (BLNG1), tapasin (tapasin), Ralcds-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyltr)	
249	12809	25390		5.24	9.2E-02 U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
249	12809	25391		5.24	9.2E-02 U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
249	12809	25392		5.24	9.2E-02 U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
2269	14843			1.58	9.2E-02 R54153.1	EST_HUMAN	yget07.1.1 Scores_Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'	
3213	15825	28302		3.92	9.2E-02 Q28831	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)	
3345	15855	28430		0.88	9.2E-02 AA534354.1	EST_HUMAN	mf79e01.1.1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:928138 3'	
3646	16249			1.16	9.2E-02 6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA	
4322	16808			1.42	9.2E-02 U82948.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region	
4398	16981			0.65	9.2E-02 BE289722.1	EST_HUMAN	60094438SF1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880178 5'	
4744	17325	28767		1.44	9.2E-02 X96402.1	NT	G.gallus Mi-CK gene	
7851	20463	33402		1.75	9.2E-02 T49820.1	EST_HUMAN	ye88c08.1.1 Strategene placenta (#837225) Homo sapiens cDNA clone IMAGE:88808 5' similar to similar to gb:X55609 GUANINE NUCLEOTIDE-BINDING PROTEIN GS, ALPHA SUBUNIT (HUMAN)	
8117	20658	33607		2.11	9.2E-02 X65258.1	NT	H. vulgaris xylose isomerase gene	
12886	24830			2.09	9.2E-02 Z22150.1	NT	S.dysgalactica fimbA gene	
448	12677	25134		2.83	9.1E-02 X78865.1	NT	O. cuniculus k12 keratin gene	
3733	16334			0.85	9.1E-02 AW372569.1	EST_HUMAN	PN2-BT0349-161289-001-f02 BT0349 Homo sapiens cDNA	
4582	17165	28508		1.55	9.1E-02 AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 54	
5505	18527	31253		1.5	9.1E-02 AF128758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, IC7, LST-1, LTb, TNF, and LTA genes, complete cds	
7420	19444	32809		11.98	9.1E-02 AW160658.1	EST_HUMAN	eu74d05.1.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'	
7688	20180	33087		0.89	9.1E-02 AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7	
7895	20204	33081		0.88	9.1E-02 U39073.1	NT	Mus musculus Tymocardin zeta mRNA, complete cds	
8855	21394	34317		1.05	9.1E-02 Y14370.1	NT	Homo sapiens gamma adducin gene, exon 9	
10325	22819			1.39	9.1E-02 T02864.1	EST_HUMAN	FB19F10 Fetal brain, Strategene Homo sapiens cDNA clone FB19F10 3' end	
10354	22848	35842		1.52	9.1E-02 S74059.1	NT	Tg616-Cy4 actin [Triplophysa gratilis=sea urchins, embryos, Genomic, 5275 nJ]	
10380	22874	35867		0.73	9.1E-02 Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes	
11653	24083			2.35	9.1E-02 8633494	NT	Bacteriophage Mu, complete genome	
11898	25038			1.62	9.1E-02 AA178901.1	EST_HUMAN	#338112-21 Strategene muscle #37209 Homo sapiens cDNA clone IMAGE:811783 3' similar to SW:TR13_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;	

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11978	24289			2.21	9.1E-02 AF052686.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12467	24877			17.53	9.1E-02 AJ281390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
12872	24740			1.6	9.1E-02 AF226888.1	NT	Bombina mori fibron heavy chain FB-H (fb-H) gene, complete cds
774	13363	26893	3.82	9.0E-02 P15328			FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP).
1678	14268	26801	6.34	9.0E-02 BF220482.1			hX38g10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178842 3' similar to contains Alu repetitive element.
2828	15381	27851	1.76	9.0E-02 AF138522.1	NT		HN-1 p8c-085-08 from USA envelope glycoprotein (env) gene, partial cds
2828	15381	27852	1.76	9.0E-02 AF138522.1	NT		HN-1 p8c-085-08 from USA envelope glycoprotein (env) gene, partial cds
3380	15858	28468	0.83	9.0E-02 AF2279135.1	NT		Dichrostomum discoideum spine coat structural protein SP85 (codE) gene, complete cds
4387	16873	29422	0.59	9.0E-02 S68757.1	NT		corticosteroid-binding globulin [Samiria sciureus-squirrel monkeys, liver, mRNA, 1474 nt]
4387	16873	29423	0.59	9.0E-02 S68757.1	NT		corticosteroid-binding globulin [Samiria sciureus-squirrel monkeys, liver, mRNA, 1474 nt]
4775	17356	28808	1.68	9.0E-02 X65740.2	NT		Plasmodium falciparum P-type ATPase 3 gene
5401	17856	30370	1.12	9.0E-02 Q24597			REGULATORY PROTEIN ZESTE
6146	18700	31519	18.48	9.0E-02 W56037.1	EST_HUMAN		z668e12 r1 Scores_fetal_lung_NihH1.10W_Homo sapiens cDNA clone IMAGE:297894 5' similar to
6820	19410		1.1	9.0E-02 BF062651.1	EST_HUMAN		PIR:S52171 S52171 small G protein - human ;
6864	18558	32428	0.77	9.0E-02 R62805.1	EST_HUMAN		7he3d03.x1 NCI CGAP_Cor16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element.
12300	24467			2.42	9.0E-02 AF022228.1	NT	
1486	14079	26817	1.46	8.9E-02 BF701593.1	EST_HUMAN		Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (orf1), rOrf2 (orf2), EscS (escS), EscT (escT), EscU (escU), EscD (escD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscY (escY), EscN (escN), SepQ (sepQ), Tir (tr), OrlU (orf1), >
1486	14079	26818	1.46	8.9E-02 BF701593.1	EST_HUMAN		602128c30F2 NIH MGIC_36 Homo sapiens cDNA clone IMAGE:4285591 5'
2430	14987	27571	9.68	8.9E-02 BE153572.1	EST_HUMAN		602128c30F2 NIH MGIC_36 Homo sapiens cDNA clone IMAGE:4285591 5'
4277	168653			1.79	8.9E-02 AF289055.1	NT	Arthrum angustatum AranFlo2 protein (AranFlo2) gene, partial cds
4741	17322	29762	1.91	8.9E-02 AA424887.1	EST_HUMAN		zmc3d4.s1 Scores_NihHMPU_S1 Homo sapiens cDNA clone IMAGE:708188 3'
6014	18834	31370	3.35	8.9E-02 AW452122.1	EST_HUMAN		UI-H-BH3-86-4-08-0-UJ.s1 NCI CGAP_Subs Homo sapiens cDNA clone IMAGE:3068294 3'
6014	18834	31371	3.35	8.9E-02 AW452122.1	EST_HUMAN		UI-H-BH3-86-4-08-0-UJ.s1 NCI CGAP_Subs Homo sapiens cDNA clone IMAGE:3068294 3'
6026	18845	31387	3.24	8.9E-02 11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA	
7244	19773	32630	1.78	8.8E-02 P47259			FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7559	20077		2.15	8.8E-02 Z78021.1	NT		H.sapiens flow-sorted chromosome 8 HindIII fragment, SC8pa20F8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (NNOS) (NNOS)
7994	20536	33439	0.89	8.9E-02	P28475	SWISSPROT (CONSTITUTIVE NOS)(NC-NOS)(BNOS)	
8072	20614	33628	0.69	8.9E-02	BF701865.1	EST_HUMAN	60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285627 5'
8072	20614	33529	0.69	8.9E-02	BF701865.1	EST_HUMAN	60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285627 5'
8534	21073	33983	4.81	8.9E-02	AA308919.1	EST_HUMAN	EST180187 Liver, hepatocyte/cellular carcinoma Homo sapiens cDNA 5' end
8538	22038	34688	0.83	8.9E-02	AI285627.1	EST_HUMAN	q556c05.1N1_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:18888830 3' similar to contains MER10.b1
8538	22038	34689	0.83	8.9E-02	AI285627.1	EST_HUMAN	MER10 repetitive element; q556c05.1N1_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:18888830 3' similar to contains MER10.b1
8648	22147	35118	0.55	8.9E-02	AA338586.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.61	8.9E-02	P18524	SWISSPROT MYOSIN2 ISOFORM	
11872	24224		4.62	8.9E-02	BP0886918.1	EST_HUMAN	602129832F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4288180 5'
12044	24330		3.07	8.9E-02	BB890220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hmch), mRNA
12307	25104		1.57	8.9E-02	U40483.1	NT	Ceratitis capitata minRNA transposon transposase gene, complete cds
1416	14009	26538	1.36	8.8E-02	Q27474	SWISSPROT PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])	
3971	16569	29038	1.08	8.8E-02	AA286128.1	EST_HUMAN	EST11565 Uterus Homo sapiens cDNA 5' end
4106	16700		4.3	8.8E-02	000268	SWISSPROT TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFI1-135)(TAFI1-130)	
4390	16978		0.98	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (sninula, keratinite) (PAX6), isoform b, mRNA
8918	21456	34376	1.18	8.8E-02	AA151672.1	EST_HUMAN	Zm88a05.s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:5682288 3'
10867	23511	38543	3.11	8.8E-02	BE284455.1	EST_HUMAN	6011191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35359848 5'
10867	23511	38544	3.11	8.8E-02	BE284455.1	EST_HUMAN	6011191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35359848 5'
11142	23850	36682	10.91	8.8E-02	AL040128.1	EST_HUMAN	DKF7p43AD1313_r1 494 (synonym: hteas3) Homo sapiens cDNA clone DKF7p43AD1313 5'
11948	24277	31019	1.73	8.8E-02	Z1561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3758	16357	28820	3.9	8.7E-02	U62885.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BCGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3758	16357	28827	3.9	8.7E-02	U62885.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BCGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	29847	1.42	8.7E-02	AF178838.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5284	17826		1.2	8.7E-02	AE000885.1	NT	Methanobacterium thermoautotrophicum from bases 1178181 to 1189408 (section 101 of 148) of the complete genome
5517	18149	30561	5.18	8.7E-02	AA288875.1	EST_HUMAN	ZS55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5517	18149	30562	5.18	8.7E-02 AA286875.1	EST_HUMAN	2s55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'		
6831	18690	32421	0.76	8.7E-02 AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14		
6831	18690	32422	0.75	8.7E-02 AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14		
7803	20346		0.46	8.7E-02 AA284532.1	EST_HUMAN	2s20e03.s1 Soces ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'		
8462	20692	33910	0.64	8.7E-02 AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 329 of the complete genome		
8452	20692	33911	0.64	8.7E-02 AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 329 of the complete genome		
10580	23125		2.71	8.7E-02 LD4758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end		
11191	23698	36745	1.77	8.7E-02 AJ007783.1	NT	Glucorubrater oxidans tRNA-Ile and tRNA-Ala genes		
11835	24289		2.35	8.7E-02 X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease		
12142	24389		2.72	8.7E-02 8879057	NT	Mus musculus nitrogen 2 (Nid2), mRNA		
1295	13889	28412	6.51	8.6E-02 AJ271738.1	NT	Humano sapiens Xq pseudautosomal region; segment 2/2		
2286	14680	27435	2.47	8.6E-02 BE409887.1	EST_HUMAN	601304016F1 NIH_MCC_21 Homo sapiens cDNA clone IMAGE:3839843 5'		
3222	15834	28312	2.42	8.6E-02 L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds		
3708	18207		4.02	8.6E-02 AF153382.1	NT	Dicyostelium discoideum adenylyl Cyclase (actA) gene, complete cds		
4584	17167	28810	0.59	8.6E-02 U68178.1	NT	Oryctolagus cuniculus galactin-3 gene, untranslated exon and 5' flanking region		
6244	18853	31624	5.78	8.6E-02 Y10829.1	NT	Homeo sapiens LCN1b gene		
6512	19112	31890	1.58	8.6E-02 J00440.1	NT	Mouse germline IgM chain gene, D region; D-q32, mu switch region (part a)		
6512	19112	31890	1.58	8.6E-02 J00440.1	NT	Mouse germline IgM chain gene, D region; D-q32, mu switch region (part a)		
7581	20086	32874	1.14	8.6E-02 P14618	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)		
7871	20413	33319	1.23	8.6E-02 5730068	NT	Homeo sapiens Smf2-related C8P activator protein (SRCAP) mRNA		
7871	20413	33320	1.23	8.6E-02 5730068	NT	Homeo sapiens Smf2-related C8P activator protein (SRCAP) mRNA		
8015	20557	33460	0.76	8.6E-02 11427428	NT	Homeo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA		
8073	20615		0.65	8.6E-02 U60198.1	NT	Dicyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds		
8852	22151	35121	1.18	8.6E-02 AF111170.3	NT	Homeo sapiens 14q32.3 Jagged2 gene, complete cds; and unknown gene		
8868	22187		1.27	8.6E-02 AW862153.1	EST_HUMAN	Hi20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972848 3'		
10057	22552	35547	0.74	8.6E-02 AF026504.1	NT	Rattus norvegicus SFA-1 like protein p1284 mRNA, complete cds		
10824	23045	36360	1.68	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product		
10824	23045	36361	1.68	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product		
11128	23438	36877	4.74	8.6E-02 BF305806.1	EST_HUMAN	601883437F1 NIH_MIGC_17 Homo sapiens cDNA clone IMAGE:4136216 5'		
11128	23438	36878	4.74	8.6E-02 BF305806.1	EST_HUMAN	601883437F1 NIH_MIGC_17 Homo sapiens cDNA clone IMAGE:4136216 5'		
111315	23013	36822	7.58	8.6E-02 AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome		
2440	15007	27578	2.52	8.5E-02 AE000852.1	NT	Helicobacter pylori 266895 section 130 of 134 of the complete genome		

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5985	18507			1.91	8.5E-02	PO8089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6162	18776	31537	5.84	8.5E-02	AF235885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds	
6942	21081	34002	1.76	8.5E-02	8754779	NT	Mus musculus myosin XV (Myo15), mRNA	
9750	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-d05 OT0037 Homo sapiens cDNA	
9750	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-d05 OT0037 Homo sapiens cDNA	
10379	22873	35868	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA	
11035	23549		12.56	8.5E-02	AF155610.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds	
11050	23663	36598	4.42	8.5E-02	AB0014562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds	
12454	24614		5.89	8.5E-02	AJ005886.1	NT	Antithrombin major mRNA for MYB-related transcription factor	
12536	24647		2.27	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA clone IMAGE:3435325	
2890	15474	27816	3.71	8.4E-02	W68330.1	EST_HUMAN	zb44e11.1r1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:3435325	
5200	17785		1	8.4E-02	X01472.1	NT	Drosophila melanogaster cap-like element 17.6	
53689	17829	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA	
55115	18147	30559	8.48	8.4E-02	BE287153.1	EST_HUMAN	601190438f1 NIH_M43C_7 Homo sapiens cDNA clone IMAGE:35343985	
6781	18382	32187	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds	
7972	20514	33421	7.35	8.4E-02	BE095074.1	EST_HUMAN	CMU-BT0780-280400-162-d05 BT0780 Homo sapiens cDNA	
8778	21315	34237	1.13	8.4E-02	AF211880.1	NT	Homo sapiens actinin precursor (ATRN) gene, exon 2	
10285	22780	35747	1.61	8.4E-02	AI75184.1	EST_HUMAN	ss8g10.1r1 Berstede codon HPLR87 Homo sapiens cDNA clone IMAGE:23359423' similar to TR:088312	
11898	24217	31042	1.92	8.4E-02	RT0408.1	EST_HUMAN	O88312 GOB-4.;	
2098	14637	27208	2.08	8.3E-02	58335680	NT	y83h12.1r1 Soares_pleasant Nb2/HF Homo sapiens cDNA clone IMAGE:1458955'	
2098	14637	27209	2.08	8.3E-02	58335680	NT	bodes hexagonus mitochondrial, complete genome	
3682	16255	28728	8.98	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN IMG309 HOMOLOG PRECURSOR	
3680	16281	28748	0.68	8.3E-02	AI436797.1	EST_HUMAN	the82g06_x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:21252103'	
3680	16281	28749	0.68	8.3E-02	AI436797.1	EST_HUMAN	the82g06_x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:21252103'	
54118	17873		1.71	8.3E-02	AW902857.1	EST_HUMAN	QY2-NN1025-030500-173-d04 NN1025 Homo sapiens cDNA	
6408	18008	31791	0.89	8.3E-02	AI942938.1	EST_HUMAN	w078f11_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:24615813'	
6504	19104	31889	3.05	8.3E-02	AF052883.1	NT	Homo sapiens protocadherin 43 gene, exon 1	
7822	20464	33371	3.57	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds	
7835	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	cg81f10_s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:14554223' similar to contains L1.L1.L1.L1	
8241	20782		4.14	8.3E-02	AA867873.1	EST_HUMAN	cg88g08_s1 NCI_CGAP_Kid5 Homo sapiens cDNA 3' similar to TR:0153392 Q15332 GAMMA	
9457	21883	34365	1.55	8.3E-02	AW5833503.1	EST_HUMAN	Subunit of sodium POTASSIUM ATPASE LIKE :	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
8470	21889		1.94	8.3E-02 AL161585.2	NT		Arribalzaga thaliana DNA chromosome 4, coding fragment No. 91
10244	22739		0.56	8.3E-02 AF020409.1	NT		Dicytostelium discoideum Daca (daca) mRNA, complete cds
11550	23898	37070	1.7	8.3E-02 AA700738.1	EST HUMAN		Zf62d04_s1 Scores_fetal_liver_spliced_INFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element;
11953	25040		1.38	8.3E-02 BE858458.1	EST HUMAN		601644770F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:39228889 5'
1421	14014		9.32	8.2E-02 Y08170.2	NT		Gallus gallus mRNA for OBCAM protein gamma isoform
1542	14134	28688	1.79	8.2E-02 AF167077.2	NT		Cantis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3108	15724		2.23	8.2E-02 AL163208.2	NT		Homo sapiens chromosome 21 segment HS21C008
3874	18472		1.68	8.2E-02 AL161498.2	NT		Arribalzaga thaliana DNA chromosome 4, coding fragment No. 10
4078	18875	28198	1.28	8.2E-02 AL163208.2	NT		Homo sapiens chromosome 21 segment HS21C008
4371	18658	28400	7.78	8.2E-02 P48890	SWISSPROT		LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	18658	28401	7.78	8.2E-02 P48890	SWISSPROT		LEUCOCYTE ANTIGEN CD97 PRECURSOR
4971	18658	28402	7.78	8.2E-02 P48890	SWISSPROT		LEUCOCYTE ANTIGEN CD97 PRECURSOR
5240	17804	30225	3.53	8.2E-02 U78008.1	NT		Mus musculus zinc transporter (Znt-3) gene, complete cds
5400	17958	30369	0.9	8.2E-02 AU110830.1	EST_HUMAN		AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1008744 5'
5538	18170	30585	1.62	8.2E-02 BE897030.1	EST_HUMAN		601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7082	18883	32502	3.11	8.2E-02 AF308555.1	NT		Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8707	21248	34169	2.98	8.2E-02 AW875128.1	EST_HUMAN		RC22PT0004-031288-011-005 PT0004 Homo sapiens cDNA clone
8817	22017	34874	4.98	8.2E-02 X04197.1	NT		Beef necrotic yellow vein virus RNA-2
8878	22177	35152	2.2	8.2E-02 BE254318.1	EST_HUMAN		601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
11858	24281	31023	5.69	8.2E-02 AE002248.2	NT		Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome
12283	24806		4.6	8.2E-02 AF275388.1	NT		Mus musculus epidermal growth factor receptor (Egrf) gene, exons 5 through 28, and complete cds, alternatively spliced
56239	18551	31278	1.08	8.1E-02 AE004008.1	NT		Xylella fastidiosa, section 152 of 229 of the complete genome
65116	18116	31908	0.97	8.1E-02 T11532.1	EST_HUMAN		A1484F Heart Homo sapiens cDNA clone A1484
7248	18777		0.72	8.1E-02 AL163278.2	NT		Homo sapiens chromosome 21 segment HS21C0079
7582	20097		1.03 -	8.1E-02 AI689281.1	EST_HUMAN		wt85f08X1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:22338503 3'
8281	20822	33741	0.62	8.1E-02 11428974	NT		Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8281	20822	33742	0.62	8.1E-02 11428974	NT		Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8828	22324		1.7	8.1E-02 AY005150.1	NT		Homo sapiens extracellular glycoprotein lactitin precursor, gene, complete cds
11371	23823	36888	1.87	8.1E-02 AL163202.2	NT		Homo sapiens chromosome 21 segment HS21C002
6	15405	25143	9.1	8.0E-02 AW854653.1	EST_HUMAN		EST388723 MAGE mesequences, MAGC Homo sapiens cDNA
971	13582	26005	1.13	8.0E-02 U80315.1	NT		Molluscum contagiosum virus subtype 1, complete genome
1738	15449	26889	10.86	8.0E-02 D28535.1	NT		Human gene for dihydrofolate reductase, complete cds (exon 1-15)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1738	15449	28870	10.86	8.0E-02	D285335.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exons 1-15)
1947	14531	27087	3.32	8.0E-02	BE097219.1	EST_HUMAN	PW3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA, mRNA
2413	14861	27556	1.14	8.0E-02	D80515.1	NT	Synochaeotis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2413	14981	27557	1.14	8.0E-02	D80515.1	NT	Synochaeotis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2509	15073		4.88	8.0E-02	BF246744.1	EST_HUMAN	801855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075819.5
2847	13753	26243	0.87	8.0E-02	MP23449.1	NT	Dicytostelium discoidineum cyclic nucleotide phosphodiesterase gene, complete cds
2925	15541	28016	0.84	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3888	18487	28848	0.59	8.0E-02	AW986118.1	EST378191 IMAGE sequences, MAGI Homo sapiens cDNA	
4146	16738		0.95	8.0E-02	4503634	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1L2) mRNA
4850	17465	28820	2.28	8.0E-02	AI434202.1	EST_HUMAN	#31g022x1 NCI_CGAP_Gene4 Homo sapiens cDNA clone IMAGE:2132114.3'
4839	17514		5.81	8.0E-02	X72784.1	NT	M.musculus gene for gelatinase B
6051	18869	31408	3.07	8.0E-02	AF276848.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18869	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8059	20611	33524	3.68	8.0E-02	AL144883.1	NT	Botryosphaeraea strain T4 cDNA library under conditions of nitrogen deprivation
9311	21625	34773	1.22	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
9311	21625	34774	1.22	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
10083	22538	0.57	8.0E-02	AL163209.2	NT	Human segment HS21C008	
10571	23203	36216	3.69	8.0E-02	AF217798.1	NT	Drosophila genome head/neck region
11983	24302	30988	3.3	8.0E-02	AJ005315.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12585	16738		3.88	8.0E-02	4503634	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1L2) mRNA
2218	14753	27588	4.15	7.9E-02	BE25008.1	EST_HUMAN	800933191TF1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858510.5
3007	15623	28101	11.7	7.9E-02	AL582028.1	EST_HUMAN	er98c08_x1 Barthead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646.3' similar to gb:Z238878
							60S RIBOSOMAL PROTEIN L38 (HUMAN).
3685	16453	28827	0.92	7.9E-02	AF030694.2	NT	Plasmid feliscatum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (ctr), CG9 (cg9), CG1 (cg1), CG6 (cg6), C32 (cg2), and C37 (cg7) genes, complete cds
3917	16515	28878	3	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	28879	3	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4834	17509		1.36	7.9E-02	AB090819.1	NT	Arribidopsis thaliana RXW24L mRNA, partial cds
6339	17948	30360	0.58	7.9E-02	AF035872.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
5339	17948	30361	0.58	7.9E-02	AF035872.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6788	18369		1.08	7.9E-02	BF368010.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GR0042 Homo sapiens cDNA
7875	20517	33424	3.32	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Sm4p (SMT4) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8941 22498	35412	4.71	7.8E-02 AI081644.1	EST_HUMAN	our33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2 CE08611;		
8941 22498	35413	4.71	7.8E-02 AI081644.1	EST_HUMAN	our33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2 CE08611;		
12479 24813		1.42	7.8E-02 AI781639.1	EST_HUMAN	wg88n10.1x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370987 3' acc89d02.56 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.L3 L1 repetitive element;		
1252 13849	23395	1.36	7.8E-02 AI783275.1	EST_HUMAN	acc89d02.56 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.L3 L1 repetitive element;		
1252 13849	23396	1.36	7.8E-02 AI783275.1	EST_HUMAN	EST_HUMAN		
4812 17487	28943	0.67	7.8E-02 BE836331.1	EST_HUMAN	PM3-FN0058-140700-0005-809 FN0058 Homo sapiens cDNA clone IMAGE:2856983 5'		
5247 18412		2.77	7.8E-02 BE250048.1	EST_HUMAN	600943055F1 NIH_NIGC_15 Homo sapiens cDNA clone IMAGE:2856983 5'		
7136 19475	32297	1.34	7.8E-02 U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORFF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds		
7136 19476	32298	1.34	7.8E-02 U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORFF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds		
8720 21259	34179	1.46	7.8E-02 BE897947.1	EST_HUMAN	601140438F1 NIH_NIGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'		
8813 21352	34274	0.6	7.8E-02 X78344.1	NT	S.cerevisiae CAT8 gene		
8893 21521	34447	0.63	7.8E-02 AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds		
8893 21521	34448	0.63	7.8E-02 AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds		
9263 21883	34828	1.08	7.8E-02 AA468954.1	EST_HUMAN	nc88b08.11 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:771731		
9717 22215	35180	0.5	7.8E-02 Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21) from 3888281 to 4214814		
10544 23081	36094	1.87	7.8E-02 U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds		
12384 24550	30890	1.85	7.8E-02 U72847.1	NT	Homo sapiens envelopakin (EVPL) gene, exons 16 through 18		
1444 15442	28598	0.91	7.7E-02 AF181987.1	NT	Homo sapiens WRN (WRN) gene, complete cds		
3847 16250		2.62	7.7E-02 AJ228983.1	NT	Homo sapiens par6A-4 gene, exons 2 to 7 and Alu repeat elements		
5129 17701	30135	0.92	7.7E-02 AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13		
7850 20392	33395	5.93	7.7E-02 AA402949.1	EST_HUMAN	ZU53d11.11 Scores over tumor NH3OT Homo sapiens cDNA clone IMAGE:7417175 similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;		
9749 22247	35229	5.97	7.7E-02 F38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C		

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22532	35527	0.75	7.7E-02	AI318862.1	EST_HUMAN	ts80168831 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z22887860S RIBOSOMAL PROTEIN L38 (HUMAN);
10037	22532	35528	0.75	7.7E-02	AI318862.1	EST_HUMAN	ts80168831 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z22887860S RIBOSOMAL PROTEIN L38 (HUMAN);
10889	23410	38428	4.97	7.7E-02	11422757 NT	Homo sapiens KIAA0028 gene product (KIAA0028), mRNA	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
12184	24884		1.81	7.7E-02	11435859 NT	Homo sapiens IMAGE:265F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3684903 5'	6013164265F1 NIH_MGC_8 Homo sapiens cDNA 5' end similar to protocadherin 43
3434	16042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to protocadherin 43
3495	16032	28537	0.87	7.6E-02	AA298447.1	EST_HUMAN	Homosapiens ASCL3 gene, CTCF1 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
3615	16218	28897	0.87	7.6E-02	AI400977.1	NT	RC3-CT0347-1103800-014-e05 CT0347 Homo sapiens cDNA
4983	17597		2.04	7.6E-02	AW58844.1	EST_HUMAN	en25g02_x1 Giesler Wilms tumor Homo sapiens cDNA clone IMAGE:1689750 3'
6247	18853	31627	0.7	7.6E-02	AI051275.1	EST_HUMAN	en25g02_x1 Giesler Wilms tumor Homo sapiens cDNA clone IMAGE:360984015
6497	18093	31682	0.83	7.6E-02	BE370328.1	EST_HUMAN	Homosapiens SCL gene locus
8292	21682	34639	1.24	7.6E-02	AJ131016.1	NT	Campylobacter jejuni NCTC1168 complete genome; segment 543
9811	22309		1.7	7.6E-02	AL139078.2	EST_HUMAN	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10120	22815	35606	0.52	7.6E-02	BE708002.1	EST_HUMAN	601654815R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:36898103'
10251	22740		0.49	7.6E-02	BE959638.2	EST_HUMAN	Lescutellum mRNA for those phosphate translocator
10480	22974	35981	0.72	7.6E-02	XO2058.1	NT	Lescutellum mRNA for those phosphate translocator
10480	22874	35882	0.72	7.6E-02	XO2058.1	NT	Lescutellum mRNA for those phosphate translocator
11523	23874	37044	2.58	7.6E-02	AW988345.1	EST_HUMAN	QV3-BN0046-150400-151-d04 BN0046 Homo sapiens cDNA
817	13435	25940	1.18	7.5E-02	5602093 NT	I	Homosapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
817	13435	25841	1.18	7.5E-02	5602093 NT	I	Homosapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
817	13435	25841	1.18	7.5E-02	5602093 NT	I	Homosapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4606	17169	28636	0.57	7.5E-02	AB015981.1	NT	W52602_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8280	20821	33740	1.15	7.5E-02	AI884367.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
8444	20984	33899	1.18	7.5E-02	AU116913.1	EST_HUMAN	7681685_x1 NCI_CGAP_Pf28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;
8845	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10387	22881	35875	0.9	7.5E-02	BF206808.1	EST_HUMAN	C_fimi DSM_201113_16S rRNA
10481	22875	35883	0.71	7.5E-02	X78480.1	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
503	13135	25623	1.23	7.4E-02	AW838547.1	EST_HUMAN	Equine herpesvirus 4 strain NS80367, complete genome
1509	14101		0.97	7.4E-02	AF030027.1	NT	

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	15178			1.04	7.4E-02	6755069 NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3854	16257	28728		0.84	7.4E-02	AI807885.1 EST HUMAN	wf43h01.x1 Scores_ NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4814	17352	28844		1.33	7.4E-02	L78810.1 NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17488	28842		2.82	7.4E-02	6978442 NT	Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
5052	17625			1.65	7.4E-02	AE000888.1 NT	Methanobacterium thermophilicum from bases 1070134 to 1088763 (section 82 of 148) of the complete genome
5076	17649	30080		1.67	7.4E-02	6878492 NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchp), mRNA
5393	17951	30384		0.93	7.4E-02	AJ012468.1 NT	Ceenorhabditis elegans mRNA for DYS-1 protein, partial
6621	18218			1.84	7.4E-02	R17477.1 EST HUMAN	Yg14g08.11 Scores_ Infant brain 1NIIB Homo sapiens cDNA clone IMAGE:323239 5'
7485	20098	32874		0.88	7.4E-02	AA65132.1 EST HUMAN	ns71d022.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20384	33288		1.23	7.4E-02	BE880112.1 EST HUMAN	601493388F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3895284 5'
8438	20878	33893		1.2	7.4E-02	U58098.1 NT	Human periodic tryptophan protein 2 (PWIP2) gene, exons 15 to 21, and complete cds
9083	21629	34568		0.92	7.4E-02	AW628805.1 EST HUMAN	hs67d11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887881 5' similar to SW:SCA2_HUMAN
9083	21629	34567		0.92	7.4E-02	AW628805.1 EST HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9380	20289	33197		0.72	7.4E-02	AI872839.1 EST HUMAN	hs67d11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887881 5' similar to SW:SCA2_HUMAN
9380	20289	33198		0.72	7.4E-02	AI872839.1 EST HUMAN	hs67d022.x1 Scores_Dickgraefse_cation_NHCD Homo sapiens cDNA clone IMAGE:2346818 3'
9728	22226	35203		0.85	7.4E-02	U622288.1 NT	Human LIM-kinase 1 and alternatively spliced LIM-kinase 1 (LIMK1) gene, complete cds
11800	24043			1.57	7.4E-02	U889282.1 NT	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
11912	24250			1.26	7.4E-02	11525893 NT	Homosapiens Histone deacetylase 5 (NC-CD-8), mRNA
12187	25015			4.44	7.4E-02	AW379431.1 EST HUMAN	CM4-HT0249-081198-037-d111 HT0243 Homo sapiens cDNA
12351	24531	30928		2.8	7.4E-02	BF035098.1 EST HUMAN	601453813F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857738 5'
12361	24535	30901		1.37	7.4E-02	AJ22459.2 NT	Aspergillus nidulans pmd. pmX, pma genes
484	13127	25613		1.42	7.3E-02	BE984981.2 EST HUMAN	6016587288R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:38886208 3'
494	13127	25614		1.42	7.3E-02	BE984981.2 EST HUMAN	6016587288R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:38886208 3'
713	13334	25820		2.68	7.3E-02	AE001789.1 NT	Thermotoga maritima section 101 of 136 of the complete genome
1528	15444	26859		4.47	7.3E-02	AW900281.1 EST HUMAN	CM0-NM1004-130300-284-008 NM1004 Homo sapiens cDNA
1885	15453			16.16	7.3E-02	AL1633022 NT	Homosapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBVGS1A1T, TCRBV7S1AIN2T, TCRBV5S1A1T, TCRBV13S1A1T, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBVGS2A2PT, TCRBV7S2A1N4T, TCRBV13S81SS>
3898	18437			0.59	7.3E-02	U68059.1 NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5137	17709			1.11	7.3E-02	U12283.1 NT	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6560	19178	31978	1.58	7.3E-02 AA179977.1	EST_HUMAN	[224e02] 61 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:1.02426 26S PROTEASE SUBUNIT 4 (HUMAN);	
7484	20037	32872	4.38	7.3E-02 PO5143	SWISSPROT	PROLINE-RICH PROTEIN MP-3	
7484	20037	32873	4.38	7.3E-02 PO5143	SWISSPROT	PROLINE-RICH PROTEIN MP-3	
8109	20850		1.08	7.3E-02 7682107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA	
9137	21672		1.38	7.3E-02 AB011930.1	NT	[224e02] 61 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:1.02426 26S PROTEASE SUBUNIT 4 (HUMAN);	
1105	19178	31978	3.07	7.3E-02 AA179977.1	EST_HUMAN	[224e02] 61 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:1.02426 26S PROTEASE SUBUNIT 4 (HUMAN);	
125	12794	25279	1.38	7.2E-02 AE000882.1	NT	Methanobacterium thermophilicum from bases 1028155 to 1038934 (section 88 of 148) of the complete genome	
125	12794	25280	1.38	7.2E-02 AE000882.1	NT	Methanobacterium thermophilicum from bases 1028155 to 1038934 (section 88 of 148) of the complete genome	
1524	14116	26852	2.11	7.2E-02 AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101	
1524	14116	26853	2.11	7.2E-02 AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101	
2685	15148		2.78	7.2E-02 U14794.1	NT	Human immunodeficiency virus type 1 isolates 26 reverse transcriptase (pol) gene, internal fragment, partial cds	
3854	16552	28021	0.59	7.2E-02 AW288322.1	EST_HUMAN	U+H-BW0-4-05-0-UI.51 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'	
4438	17024	29484	3.65	7.2E-02 BF572307.1	EST_HUMAN	802077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'	
5223	17788	30207	0.89	7.2E-02 AB001662.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds	
5491	18125	30533	2.8	7.2E-02 U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome	
5492	18126	30534	8.6	7.2E-02 P11120	SWISSPROT	CALMODULIN	
62265	18873		0.83	7.2E-02 BF217698.1	EST_HUMAN	801885805F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098224 5'	
72220	18751	32007	1.27	7.2E-02 BF216086.1	EST_HUMAN	80188558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098710 5'	
7261	19789		1.54	7.2E-02 5834697	NT	Strongylocentrotus purpuratus mitochondrial, complete genome	
8128	20689	33578	0.69	7.2E-02 P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3	
8128	20689	33579	0.69	7.2E-02 P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3	
8894	21532		0.5	7.2E-02 Y17217.1	NT	Lactococcus lactis capE gene	
9495	21995		0.57	7.2E-02 X16340.1	NT	Human gene for sex hormone-binding globulin (SHBG)	
9529	22026	34988	2.28	7.2E-02 AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUC01 5'	
9874	22173	35149	4.69	7.2E-02 L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds	
9828	22326	35307	1.01	7.2E-02 BF125389.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'	
9914	22410	35386	2.73	7.2E-02 AW873187.1	EST_HUMAN	hp24f11X1 NCI CGAP_Ad1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q8Z340 Q8Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;	

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HK BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Descriptor
10254	22749	35737	2.11	7.2E-02	U82885.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	
10370	22884	35857	6.88	7.2E-02	BE565003.1	EST_HUMAN	601343028F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685851 5'	
10392	22889		3.22	7.2E-02	BE538214.1	EST_HUMAN	601065104F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451589 5'	
10792	23115	38824	6.18	7.2E-02	AF048874.1	NT	Rattus norvegicus bHLH transcription factor Mash1 (Mst1) gene, complete cds	
11622	24182	31033	1.54	7.2E-02	AA773686.1	EST_HUMAN	af81ad41.1 Scareas_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1048389 5'	
11857	24210		4.88	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Scareas_P) Homo sapiens cDNA clone PS13D5 3'	
11914	24252		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc005808.s1 NCI_CGAP_Pheri Homo sapiens cDNA clone IMAGE:1098839 3'	
11979	24280		3.69	7.2E-02	U82828.1	NT	Homo sapiens atotide tokanglechesis (ATM) gene, complete cds	
11985	24858		7.52	7.2E-02	AW800982.1	EST_HUMAN	CMA4-NI009-200300-118-c11 NI1009 Homo sapiens cDNA	
12514	24833		1.65	7.2E-02	AA401779.1	EST_HUMAN	z557c12.r1 Scareas_mensis_NHT Homo sapiens cDNA clone IMAGE:728454 5'	
1948	14532	27088	1.42	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene, partial cds	
2331	14902	27473	4.53	7.1E-02	BF208892.1	EST_HUMAN	601187228F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082281 5'	
7848	20390	33292	0.84	7.1E-02	AI125284.1	EST_HUMAN	qd32a10.x1 Scareas_nestis_NHT Homo sapiens cDNA clone IMAGE:1738922 3'	
11700	24113		6.04	7.1E-02	BE504784.1	EST_HUMAN	601143074F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'	
554	13185	25863	0.97	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR	
1547	14139		1.43	7.0E-02	X08877.1	NT	Mantis religiosa Mfcat-1 gene	
1798	14389	26833	0.94	7.0E-02	AA058943.1	EST_HUMAN	Z6804.s1 Stratego colon (#037204) Homo sapiens cDNA clone IMAGE:509509 3'	
3064	15680	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	UH-B11-0574-07-0-U_51 NCI_CGAP_Sub3 Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S	
3988	16584	28933	1.71	7.0E-02	AA816438.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);	
4118	16712	28166	1.11	7.0E-02	BED70284.1	EST_HUMAN	QV4-BT0407-280100-080-610 BT0407 Homo sapiens cDNA	
4219	16807		1.11	7.0E-02	AW792862.1	EST_HUMAN	CMA4-UH0001-080300-270-812 UMP001 Homo sapiens cDNA	
4294	16880	28827	1.28	7.0E-02	AF077821.1	NT	Caris familiaris inducible nitric oxide synthase mRNA, complete cds	
5003	17633	30978	9.58	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050071 5'	
5580	18211		0.84	7.0E-02	Y09143.2	NT	Lumbatus rubellus mRNA for cryptophillin B	
7431	18655	3220	0.88	7.0E-02	AV688225.1	EST_HUMAN	AV688225 GKC Homo sapiens cDNA clone GKCCAAED8 5'	
8027	21564	34483	1.41	7.0E-02	9828113	NT	African swine fever virus, complete genome	
8515	22015	34973	1.25	7.0E-02	K02801.1	NT	Rat Ig gammaine epsilon H-chain gene C-region, 3' end	
8883	22360	35340	0.73	7.0E-02	U27268.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds	
11251	23781	36837	2.68	7.0E-02	AA724295.1	EST_HUMAN	eh3806.s1 Scareas_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:1.14837 TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);	

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25649	11.84	6.8E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25850	11.84	6.8E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.8E-02	4507868	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3860	16458	28921	1.16	6.8E-02	Q106384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3860	16458	28922	1.16	6.8E-02	Q106384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5381	17940	30354	3.58	6.8E-02	AF121254.1	NT	Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (BglB), beta-glucosidase specific transport protein (BglS), transcription antiterminator (BglTR), enterocin B precursor (entB), enteroch B immunity protein
79086	20538		1.13	6.8E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8488	21027	33944	1.1	6.8E-02	BE567435.1	EST_HUMAN	60134081(F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:36883090 5'
8488	21027	538945	1.1	6.8E-02	BE567435.1	EST_HUMAN	60134081(F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:36883090 5'
9048	21595	34518	0.61	6.8E-02	U22867.1	NT	Barberie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11853	24213		17.91	6.8E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
12031	24321		1.86	6.8E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCH HOMOLOG
12258	24468		3.68	6.8E-02	AF185853.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEPP2) gene, complete cds
1828	14511	27065	1.83	6.8E-02	AA498759.1	EST_HUMAN	883072.1 Cestier Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M223382
1828	14511	27066	1.83	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); 883072.1 Cestier Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M223382
1828	14511	27068	1.83	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); 883072.1 Cestier Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M223382
1850	14534	27090	3.99	6.8E-02	AF156873.1	NT	Homo sapiens putative hepatic transcription factor (WESCR14) gene, complete cds
2023	14805	27170	1.68	6.8E-02	BE283781.1	EST_HUMAN	601164141(F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5'
4651	17233		0.86	6.8E-02	BE141076.1	EST_HUMAN	MRO-H10089-071089-001-005 HT10089 Homo sapiens cDNA
6680	19478		4.62	6.8E-02	BE091890.1	EST_HUMAN	RC1-BT0254-080300-017-d09 BT10254 Homo sapiens cDNA
7324	18851	32713	6.08	6.8E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8230	20771	33680	5.36	6.8E-02	AJ248267.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8230	20771	33681	5.36	6.8E-02	AJ248267.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11646	25684		2.49	6.8E-02	TO3214.1	EST_HUMAN	F34A8 Fetal brain, Stratagene Homo sapiens cDNA clone F34A8 3' end similar to LINE-1
11783	24198		2.42	6.8E-02	AA758914.1	EST_HUMAN	ah87705.s1 Soares testis, NHT Homo sapiens cDNA clone 1320705 3'
12380	24547		1.37	6.8E-02	AW975939.1	EST_HUMAN	EST387948 MAGE sequences, MAGN Homo sapiens cDNA
12444	24580		2.87	6.8E-02	89105985	NT	Mus musculus latent TGF beta binding protein (Tgfbb), mRNA
12850	25098	30814	1.54	6.8E-02	89788935	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1678	14169		1.51	6.7E-02	AF115538.1	NT	Oncophyndus mykiss TAP1 protein (OncmyTAP1) mRNA, OncmyTAP1 allele, complete cds
1838	14522	27078	3.82	6.7E-02	AJ220285.1	EST_HUMAN	cp73604.X1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3780	16380	28844	4.61	6.7E-02	P17278	SWISSPROT	HOMEOPBOX PROTEIN HOX-D4 (CHOX-A)	
4842	17420	28873	3.51	6.7E-02	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14	
7782	20335	33241	0.63	6.7E-02	X62685.1	NT	H sapiens DNA for cGMP phosphodiesterase (exons 4-22)	
7782	20335	33242	0.63	6.7E-02	X62685.1	NT	H sapiens DNA for cGMP phosphodiesterase (exons 4-22)	
9518	22018	34975	0.75	6.7E-02	AW137359.1	EST_HUMAN	U1+81-act-9-01-01-U1.51 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'	
9518	22018	34976	0.75	6.7E-02	AW137359.1	EST_HUMAN	U1+81-act-9-01-01-U1.51 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'	
2225	14900	27372	3	6.8E-02	AJ282241.1	NT	Mus musculus Capn12 gene for captain 12, exons 1-21, three alternative transcripts	
3510	18115	26594	9.7	6.8E-02	R64308.1	EST_HUMAN	Y18810.81 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138578 3'	
3524	18128	28809	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	
3524	18128	28810	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	
4154	16748	26220	1.83	6.8E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	
5114	17888	30122	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2)	
5114	17888	30123	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2)	
5164	17753	30160	0.57	6.8E-02	AA383244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN)	
5164	17753	30161	0.57	6.8E-02	AA383244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN)	
6688	18284	32088	4.11	6.8E-02	X08411.1	NT	P. vulgaris mRNA for chalcone synthase	
7888	20430	33328	1.58	6.8E-02	AF052672.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds	
8408	20349	33868	0.72	6.8E-02	AF083055.1	NT	Dicistrovium discideum dafin (dara) gene, complete cds	
8714	21253	0.49	6.8E-02	0808673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)		
8852	21391	34212	0.52	6.8E-02	9628198	NT	Human respiratory syncytial virus, complete genome	
8852	21391	34213	0.52	6.8E-02	9628198	NT	Human respiratory syncytial virus, complete genome	
8882	22359	35329	0.58	6.8E-02	AI489762.1	EST_HUMAN	b97/g08.x1 NCI CGAP L124 Homo sapiens cDNA clone IMAGE:2149488 3'	
8889	22494	35493	1.54	6.8E-02	Y07848.1	NT	Homo sapiens EW5_g8722, np_22 and bam22 genes	
10028	22524	0.53	6.8E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA		
10842	23363	38378	7.08	6.8E-02	BF374248.1	EST_HUMAN	MR1-SN0084-010500-008-a12 SN0084 Homo sapiens cDNA	
12251	24482		2.87	6.8E-02	88317891	NT	Mus musculus DIPB gene (Dipb), mRNA	
12585	24678		1.38	6.8E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region	
608	13239	25710	1.85	6.8E-02	BF027639.1	EST_HUMAN	601671046F1 NIH MGIC 20 Homo sapiens cDNA clone IMAGE:3954178 5'	
1024	13635	28151	2.61	6.8E-02	7706988	NT	Homo sapiens E2F-like protein (LOC51270), mRNA	
1439	14028	28558	3.4	6.8E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds	
1770	14360	28905	1.42	6.8E-02	AE000784.1	NT	Aquifex aeolicus section 98 of 108 of the complete genome	
5349	17909	30324	0.88	6.8E-02	D45898.1	NT	Caenorhabditis elegans DNA for yanodine receptor, complete cds	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.79	6.5E-02	AA443091.1	EST HUMAN	Zm48h12_s1 Soares ovary tumor NBHOTT Homo sapiens cDNA clone IMAGE:756749 3' similar to gb:AM280388
6884	19280	32094	0.89	6.5E-02	BF685340.1	EST HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-5 BETA CHAIN (HUMAN); 602118837F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:42780289 5'
7051	18070	30461	0.90	6.5E-02	U22681.1	NT	Azotobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds
6854	22352	35532	0.85	6.5E-02	BE083200.2	EST HUMAN	601658817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:38856373 3'
6854	22352	35533	0.66	6.5E-02	BE083200.2	EST HUMAN	601658817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:38856373 3'
10563	22857	35949	0.59	6.5E-02	BF108300.1	EST HUMAN	601623511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043198 5'
10518	23058	36067	5.88	6.5E-02	AA195848.1	EST HUMAN	Z32055.s1 Soares_NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:885144 3'
11689	24091		6.28	6.5E-02	M21498.1	NT	Rabbit microsomal epoxide hydrolase
12040	24327		3.84	6.5E-02	AF029893.1	NT	Nectria haematoxocca kinase related protein 2 (KRP2) gene, complete cds
801	13230	25703	1.74	6.4E-02	X94549.1	NT	A cathepsin precursor of pentidin-chlorophyll-protein (PCP) gene
5841	18270	30743	1.21	6.4E-02	AI191858.1	EST HUMAN	Q807001_x1 Soares_Nests_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR&L3 LTR repetitive element;
6261	18859	31639	5.4	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gng-1) gene, complete cds
6261	18859	31640	5.4	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gng-1) gene, complete cds
6534	19134	31827	0.86	6.4E-02	AI672898.1	EST HUMAN	WE73G12_x1 Soares_Dickgraefse_odon_NHCD Homo sapiens cDNA clone IMAGE:2348790 3'
66007	19841	32477	4.7	6.4E-02	BE974448.1	EST HUMAN	601660425F2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:38950503 3'
82778	20819		2.88	6.4E-02	67533323	NT	Mus musculus chaperonin subunit beta (zeta) (Cct8), mRNA
85598	21138	34052	3.59	6.4E-02	AA0893305.1	EST HUMAN	K1419_seq.F_Human fetal heart_LambdazAP Express_Homo sapiens cDNA clone CBDAIA10
90555	21592	34522	0.85	6.4E-02	AF150185.1	EST HUMAN	AF150185 Human mRNA from cd34+ stem cells_Homo sapiens cDNA clone CBDAIA10
95008	22006		0.81	6.4E-02	BE894083.1	EST HUMAN	RC1-OT0033-150000-014-006 OT0033 Homo sapiens cDNA
98533	22123	35098	1.79	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10162	22857	35652	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10162	22857	35653	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoR α gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoR α gene, and sodium phosphate transporter (NPT3) gene, complete cds
11931	24971		4.88	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
11866	24296	30863	2.88	6.4E-02	AJ271174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1781	14981	26826	3.03	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70l gene, partial cds; smnRNP, G7A, NG23, MUSI homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3684	16208			2.41	6.3E-02	P37082	HEAT SHOCK PROTEIN 70 HOMOLOG
6285	18883	31682	1.1	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
7281	19819		1.05	6.3E-02	X97889.1	NT	H. sapiens gene encoding La autoantigen
8215	21732	34675	0.90	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
8827	22423	35397	2.86	6.3E-02	AB010162.1	NT	Hepatitis C virus RNA for poly(A)n (NSSA region), partial cds, strain: CMR-152
10172	22807		0.87	6.3E-02	AY688670.1	EST_HUMAN	AV688670 GCKCABE01 5'
10594	18883	31682	3.0	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
4337	18824	28385	3.3	8.2E-02	AL181572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
4431	17017		1.04	8.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Ncd-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds
4682	17284		6.75	8.2E-02	Q82191	NT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO52)
68889	19824	32459	0.75	8.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7623	20198	33014	0.75	8.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8877	25123		0.81	8.2E-02	ME1101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9267	21783	34742	0.5	8.2E-02	AA778450.1	EST_HUMAN	af20a08_s1 Soares_total_fetus_Nb25IF8_3yv Homo sapiens cDNA clone IMAGE:1032178 3'
9401	21910	34859	1.05	8.2E-02	68777898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2) mRNA
11027	23541	38578	1.74	8.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11226	23757	38814	1.89	8.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyt1 gene)
11770	25097		8.34	8.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12200	24426	30651	3.56	8.2E-02	BF112039.1	EST_HUMAN	737708_x1 Soares_NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:35223816 3' similar to TR-Q9Y4S6 Q8Y4S6 HYPOTHEICAL 30.3 KD PROTEIN [1];
277	12834	25220	4.8	8.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4063	16680		2.78	8.1E-02	UT3S25.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4759	17340	29788	1.09	8.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACSS) gene, complete cds
4759	17340	29787	1.09	8.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACSS) gene, complete cds
6262	18870		1.42	8.1E-02	4507070	NT	Homo sapiens SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8207	20748	33681	3.31	8.1E-02	X99238.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8595	21134	34048	0.95	8.1E-02	BE871853.1	EST_HUMAN	6016510588R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8595	21134	34049	0.95	8.1E-02	BE871853.1	EST_HUMAN	6016510588R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10608	23142	36153	6.34	8.1E-02	BE778543.1	EST_HUMAN	IL3-HT0818-110500-138-C08 HT10618 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11728	25090			23.38	6.1E-02 X703689.1	NT	S_japonicum mRNA for serine-enzyme
12317	24880			1.39	6.1E-02 AI898811.1	EST_HUMAN	t258107.x1 NCI_CGAP_O35 Homo sapiens cDNA clone IMAGE:22828901 3'
12484	24502			7.98	6.1E-02 AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
13035	13889	28419		1.01	8.0E-02 AE001177.1	NT	Thermotoga maritima section 88 of 138 of the complete genome
2700	15257	27825		1.16	6.0E-02 AW888848.1	EST_HUMAN	EST380522 MAGE-like sequences, MAGJ Homo sapiens cDNA
2801	15353			1.58	6.0E-02 AB031289.1	NT	Mesocetobius cari mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-5'c, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 4, rRNA-Gin, rRNA-Phe, tRNA-Met
2863	12777	25259		1.09	6.0E-02 AA188730.1	EST_HUMAN	2p78c04.11 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:6283105'
2863	12777	25260		1.09	6.0E-02 AA188730.1	EST_HUMAN	2p78c04.11 Strategene HeLa cell s3 837216 Homo sapiens cDNA 5' end similar to tissue-specific protein
32888	15878	28380		1.24	6.0E-02 AA3722378.1	EST_HUMAN	EST784288 Colon adenocarcinoma IV/Homo sapiens cDNA 5' end similar to tissue-specific protein
32888	15878	28381		1.24	6.0E-02 AA3722378.1	EST_HUMAN	EST784288 Colon adenocarcinoma IV/Homo sapiens cDNA 5' end similar to tissue-specific protein
36897	16298			1.01	6.0E-02 BE984443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876080 3'
5104	17676	30118		0.95	6.0E-02 2677739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
55695	18225			1.69	6.0E-02 AW370211.1	EST_HUMAN	RC3-BT0263-0111699-013-h04 BT0253 Homo sapiens cDNA
6384	18988	31746		1.43	6.0E-02 AI807537.1	EST_HUMAN	W48h05x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.H L1.L1 repetitive element;
70583	18082	30438		2.73	6.0E-02 5174688 NT	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
70583	18082	30439		2.73	6.0E-02 5174688 NT	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19788	32824		2.17	6.0E-02 BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4048228 5'
7672	20184	33072		1.84	6.0E-02 AI204275.1	EST_HUMAN	qf58h08.x1 Soares_nests_NHT Homo sapiens cDNA clone IMAGE:1754198 3'
8381	20901			0.57	6.0E-02 11488485 NT	NT	Radicofanellus americanus mitochondrion, complete genome
91186	21713	34656		1.12	6.0E-02 AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237382 3'
91186	21713	34657		1.12	6.0E-02 AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237382 3'
9327	21841	34782		2	6.0E-02 AJ245385.1	NT	Acipenser brevirostris IgM gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34793		2	6.0E-02 AJ245385.1	NT	Acipenser brevirostris IgM gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35298		0.51	6.0E-02 AA309707.1	EST_HUMAN	EST180654 Jurkat T-cells V/Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
9819	22317	35300		0.51	6.0E-02 AA309707.1	EST_HUMAN	EST180654 Jurkat T-cells V/Homo sapiens cDNA clone IMAGE:5851686 5' similar to
11214	23117			2.13	6.0E-02 AA128988.1	EST_HUMAN	zN87c03.11 Strategene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:2282891 3'
11185	24285	30982		1.43	6.0E-02 11431702 NT	NT	gb:X689181 60S RIBOSOMAL PROTEIN L31 (HUMAN); Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554			6.04	6.0E-02 AI809273.1	EST_HUMAN	wf88h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-060298 C60288 KIAA0551 PROTEIN;

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
260	12810	25303	4.76	5.0E-02	AW934719.1	EST_HUMAN	RCI-DT0001-280100-012-010 DT0001 Homo sapiens cDNA
3012	15828	28107	2.75	5.0E-02	AF180269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	28789	0.87	5.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	28800	0.97	5.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.8	5.0E-02	AF188111.1	NT	Duck pectoralis strain 90-2183 capsid protein (VP3) gene, partial cds
4886	17570	30014	0.80	5.0E-02	AF008304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
6873	24774	32374	0.67	5.0E-02	AF145680.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21091	34011	1.88	5.0E-02	9055249	NT	Mus musculus Inositol-related homobox 6 (Drosophila) (Inx5), mRNA
8372	20311		0.82	5.0E-02	BF22748.1	EST_HUMAN	6018776809FT NIH MGC_55 Homo sapiens cDNA clone IMAGE:4105884 5'
10884	23198		3.41	5.0E-02	86798870	NT	Mus musculus follistatin-like (Fst), mRNA
10889	23419	36436	2.35	5.0E-02	11433356	NT	Homo sapiens nibrin (LOC51188), mRNA
11429	23890		1.83	5.0E-02	AJ240783.1	NT	Gallus gallus HKC9 telomere junction
8688	13579		5.2	5.0E-02	D80110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1
1700	14293	26828	1	5.0E-02	Q8117688	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
22880	15504		0.98	5.0E-02	AJ223621.1	NT	Populus trichocarpa CCA-OMT1 gene, exon 11 to exon 5
3725	16238	28793	1.35	5.0E-02	AE001776.1	NT	Thermotoga maritima section 87 of 138 of the complete genome
4446	17032	28473	5.29	5.0E-02	AW051927.1	EST_HUMAN	W24c02-x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4446	17032	28474	5.29	5.0E-02	AW051927.1	EST_HUMAN	W24c02-x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4845	17227	26882	5.04	5.0E-02	AJ247505.1	EST_HUMAN	q58f01_x1 Scores fetal liver_spineen INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to q58f01_x1 Scores fetal liver_spineen INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to q58f01_x1 Scores fetal liver_spineen INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3'
4845	17227	26983	5.04	5.0E-02	AJ247505.1	EST_HUMAN	q58f01_x1 Scores fetal liver_spineen INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to q58f01_x1 Scores fetal liver_spineen INFILS_S1 Homo sapiens cDNA clone IMAGE:1848697 3'
4874	17258		1.98	5.0E-02	AF086284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5284	17890	30282	0.57	5.0E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egr1) gene, exons 5 through 28, and complete cds, alternatively spliced
6098	18895	31428	1.52	5.0E-02	AA180684.1	EST_HUMAN	q58e11_x1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:827068 3'
7670	20182	33089	2.73	5.0E-02	MB9150.1	NT	Human polymorphic microsatellite DNA
7670	20182	33070	2.73	5.0E-02	MB9150.1	NT	Human polymorphic microsatellite DNA
8901	21140	34054	0.76	5.0E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
11871	24223		2.86	5.0E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12177	25095		6.45	5.0E-02	AA604289.1	EST_HUMAN	no75e11_x1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112894 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
30893	15708	28179	1.13	5.7E-02 AI081644.1	EST_HUMAN	orf63b05.s1 NCI_CGAP_Bi2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WF:C37A22
3107	15722	28183	1.6	5.7E-02 AF119117.1	NT	CE086111; Homo sapiens dopamine transporter (SLC8A3) gene, complete cds
3798	16370		0.86	5.7E-02 AF001292.1	NT	Chromomus truttae truttae globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3871	18469	28832	2.44	5.7E-02 AW867791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
4785	17373		1.06	5.7E-02 MS85089.1	NT	Bos taurus lysosome gene (cow 3), complete cds
5334	17895	30310	0.89	5.7E-02 AJ251673.1	NT	Homo sapiens partial sterath-1 gene
60339	18858		0.8	5.7E-02 AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
80586	20637	33548	1.48	5.7E-02 AJ288690.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kvo.2 gene)
9784	22262	35245	0.65	5.7E-02 6881260	NT	Mus musculus act2 oncogene (Ec2), mRNA
11067	23579	30017	4.17	5.7E-02 AI752825.1	EST_HUMAN	cn18s09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18s09 random
11067	23579	30018	4.17	5.7E-02 AI752825.1	EST_HUMAN	cn18s09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18s09 random
11227	23733		1.58	5.7E-02 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12085	24891		12.98	5.7E-02 D50320.1	NT	PIg DNA for SPAl2, complete cds
12257	24457		1.71	5.7E-02 AJ2711735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12334	24985		3.31	5.7E-02 AF217490.1	NT	Homo sapiens fragile XQ alpha reductase (FQR) gene, exons 8, 9, and partial cds
12483	25074		8.94	5.7E-02 AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
12622	24700	30853	1.58	5.7E-02 R48513.1	EST_HUMAN	yf34d10.s1 Soares breast 2NBH1Bst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element;
1574	14167	28888	1.2	5.6E-02 AF084455.1	NT	Hydroxyle rostrinotula ribosomal protein L16 (rp16) gene, intron; chloroplast product
4746	17327	28789	1.21	5.6E-02 AB013100.1	EST_HUMAN	Lysopermeion esculentum LE-ACS6 mRNA for 1-sphingocyclopropane-1-carboxylate synthase, complete cds repetitive element; contains element L1 repetitive element;
4806	17384	28834	1.2	5.6E-02 AA200589.1	EST_HUMAN	2245c01.s1 NCI CGAP CGBP1 Homo sapiens cDNA clone IMAGE:700418 3'
6786	19358	32188	5.98	5.6E-02 AW172708.1	EST_HUMAN	x02c10.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2858050 3' similar to TR.O94978 O94978 KIAA0805 PROTEIN;
6971	19548	32372	0.9	5.6E-02 AA886182.1	EST_HUMAN	cd47112.s1 NCI CGBP1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7205	19738	32588	3.1	5.6E-02 BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8737	21278	34198	2.2	5.6E-02 BE542683.1	EST_HUMAN	601087158F1 NIH_MIGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8737	21278	34199	2.2	5.6E-02 BE542683.1	EST_HUMAN	601087158F1 NIH_MIGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'

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Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9728	22224	35201	1.07	5.6E-02 AA482864.1	EST_HUMAN	nt/40007_81 NCI_CGAP_AM1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768859 G768859	LAMINA ASSOCIATED POLYPEPTIDE 1C. ; Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11439	23869		2.33	5.6E-02 AF280225.1	NT		H. sapiens gene encoding La autoantigen
2670	15237	27804	6.14	5.6E-02 X97889.1	NT		Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
3251	15863	28345	3.83	5.6E-02 6755501	NT		Gallid herpesvirus mRNA fragment
4286	16862	28328	1.12	5.6E-02 L41561.1	NT		TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5840	18464	31188	3.19	5.6E-02 Q01174	SWISSPROT		TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6178	18464	31188	3.88	5.6E-02 Q01174	SWISSPROT		TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	18837	32802	1.77	5.6E-02 6755802	NT		Mus musculus tuftelin 1 (Tuft1), mRNA
8003	20805	33516	0.77	5.6E-02 AF170911.1	NT		Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8003	20805	33517	0.77	5.6E-02 AF170911.1	NT		Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8573	22073	35034	0.61	5.6E-02 10947034	NT		Homo sapiens eIF4E-transporter (4E-T), mRNA
9573	22073	35035	0.61	5.6E-02 10947034	NT		Homo sapiens second IL11 receptor alpha chain (IL11RA2) gene, exons 1 and 2
9884	22153	35138	1.28	5.6E-02 U69462.1	NT		Mus musculus second cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhesK), glycerol dehydrogenase (dhaD), transcriptional activator (dhesR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydrogenase (dhaS), >
10889	23418	38435	11.52	5.5E-02 U09771.1	NT		Oryza sativa rb63-1 gene for putative Bowman Birky trypsin inhibitor
30554	15870		0.85	5.4E-02 AJ277468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA	
3469	18013		6.27	5.4E-02 BE073468.1	NT		Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
3982	16580	29051	0.58	5.4E-02 U85806.1	NT		Xenopus laevis homeobox protein (Vax-1) mRNA, complete cds
5119	17691	30128	2.48	5.4E-02 U53628.1	NT		Bacillus subtilis complete genome (section 13 of 21); from 2895281 to 2813730
8067	20809		1.11	5.4E-02 Z39116.1	NT		Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9001	21538	34487	0.61	5.4E-02 AF280225.1	NT		
10578	23113	38120	1.88	5.4E-02 U20790.1	NT		Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11058	23570	36808	1.58	5.4E-02 BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA	
11058	23570	36807	1.58	5.4E-02 BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA	
11958	24882		2.9	5.4E-02 U44894.1	NT		Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13696	26205	1.98	5.3E-02 AW391248.1	EST_HUMAN	QV0-ST0213-021288-082-609 ST0213 Homo sapiens cDNA	
1091	13696	26206	1.68	5.3E-02 AW391248.1	EST_HUMAN	QV0-ST0213-021288-082-609 ST0213 Homo sapiens cDNA	
1553	14145	28979	21.63	5.3E-02 TB4759.1	EST_HUMAN	Y837112.1 Stratagene lung (#837120) Homo sapiens cDNA clone IMAGE:110951 5' similar to gb:K01506	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2541	16105	27677	2.71	5.3E-02 AJ276408.1	NT		Pseudomonas putida rgsS gene
2869	15585	28068	0.88	5.3E-02 M58417.1	NT		Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2869	15585	28067	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3187	15789	28271	4.52	5.3E-02	AJ276408.1	NT	Pseudomonas putida ttrS gene
							<i>Mus musculus</i> Scy6B, Scy6S, Scy616-ps, Scy6S genes for small inducible cytokine A6 precursor, small inducible cytokine A8 precursor, Scy16 pseudogene, small inducible cytokine A5 precursor, complete cds
5248	17811	30234	0.75	5.3E-02	AB051987.1	NT	
5250	17813	30236	8.25	5.3E-02	M804683.1	NT	<i>Mus musculus</i> caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18154	30568	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 28895 section 5 of 134 of the complete genome
5522	18154	30569	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 28895 section 5 of 134 of the complete genome
6251	18890	31832	0.71	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6894	18541	32283	4.23	5.3E-02	9895413	NT	Lymphocystis disease virus 1, complete genome
7149	19882	32523	1.55	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7396	18821		2.05	5.3E-02	ST8222.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4033 nt]
7818	20290	33189	0.52	5.3E-02	P28742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNT6-SPO11 INTERGENIC REGION
8344	20885		0.54	5.3E-02	U10098.1	NT	<i>Mus musculus</i> 12S rRNA cytbmatin C (cyt3) gene, complete cds
9053	21580	34521	1.83	5.3E-02	X03127.1	NT	<i>Podocarpus</i> serine/methionine epsilon-kinase mRNA
10038	22533	35530	0.54	5.3E-02	AB022805.1	NT	<i> Homo sapiens</i> hCMIT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10038	22533	35530	0.54	5.3E-02	AB022805.1	NT	<i> Homo sapiens</i> hCMIT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10158	22851		0.82	5.3E-02	Y07907.1	NT	Danio rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and post somitogenesis, 20-28 hpf)
10235	22730	35721	0.85	5.3E-02	X89432.1	NT	B. nana poly[cl] mRNA for transcription factor
2324	14865		110.52	5.2E-02	5031908	NT	<i> Homo sapiens</i> meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3148	15762	28228	2.4	5.2E-02	AJ277061.1	NT	<i> Homo sapiens</i> partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28228	2.4	5.2E-02	AJ277061.1	NT	<i> Homo sapiens</i> partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	10611	28064	0.7	5.2E-02	AF226101.1	NT	<i> Arabidopsis thaliana</i> putative dicarboxylate diltion protein (Crd1) mRNA, complete cds
4385	16852	28392	3.61	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nor-1 mRNA, complete cds
4846	17424	28877	1.29	5.2E-02	L33248.1	NT	Drosophila melanogaster filament protein homolog (sep1) gene, complete cds
6073	18893	31439	0.89	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6255	18864		1.42	5.2E-02	AIB30965.1	EST_HUMAN	W80404_x1 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE-2408150 3' similar to contains MER15.b1 MER15 repetitive element;
7318	19845	32706	1.19	5.2E-02	P38522	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8138	20877		1.98	5.2E-02	AL163204.2	NT	<i> Homo sapiens</i> chromosome 21 segment HS21C004
8645	22145	35113	1.97	5.2E-02	D10827.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds
8645	22145	35114	1.97	5.2E-02	D10827.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445			1.84	5.2E-02 Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513			1.27	5.2E-02 D63382.1	NT	Mouse DNA for regII gamma protein, complete cds
2402	14970			1.14	5.1E-02 AL134071.1	EST_HUMAN	DIKFZ547D073_11 547 (synonym: Mbr1) Homo sapiens cDNA clone DKFZp547D073 5'
4282	168698	28315		0.73	5.1E-02 AE001301.1	NT	Glyceraldehyde-3-phosphate dehydrogenase, section 28 of 87 of the complete genome
4808	17483	28641		8.03	5.1E-02 AF086167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5205	17770	301183		1.14	5.1E-02 BE957423.2	EST_HUMAN	601653865R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE3838381 3'
6777	183699	321182		0.76	5.1E-02 AF280369.1	NT	HIV-1 patient 88 from Italy protease (pol) gene, complete cds
6842	18630	304172		1.6	6.1E-02 BF370825.1	EST_HUMAN	Q00-UHM0051-250800-350-508 UHM0051 Homo sapiens cDNA
8185	20738	338446		0.82	5.1E-02 M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8185	20738	338447		0.82	5.1E-02 M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8288	204289	337150		1.48	5.1E-02 AJ131988.1	NT	Spodoptera littoralis mRNA for 3-dehydroxydihydroxyacetone phosphate reductase
8818	21357	34282		0.63	5.1E-02 P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELELETAL 14 (CYTOKERATIN 14) (K14) (CK14)
8818	21357	34283		0.63	5.1E-02 P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELELETAL 14 (CYTOKERATIN 14) (K14) (CK14)
9723	22221	361188		8.16	5.1E-02 AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10084	22579	35572		1.83	5.1E-02 P40863	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10708	23237	362530		2.88	5.1E-02 AF08630.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080 Homo sapiens ES18 mRNA, partial cds
10708	23237	362531		2.88	5.1E-02 AF08630.1	NT	Homo sapiens ES18 mRNA, partial cds
12232	24448			1.51	5.1E-02 AF082467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
508	13141	256228		1.78	5.0E-02 AF086304.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1246	13843	26350		6.63	5.0E-02 Z98104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080 Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-2) (PRP-2/PRP-4) (PIF-PIF-S) (PROTEIN A PROTEIN C) (CONTAINS: PEPTIDE P-C)
2034	14616	27182		3.63	5.0E-02 P02810	SWISSPROT	Oryctolagus cuniculus UDP-glucuronyltransferase (UGT2B13) mRNA, complete cds
2845	13834	28150		1.78	5.0E-02 U72742.1	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3381	15890			1.42	5.0E-02 7305810	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3835	162538			1.08	5.0E-02 U32782.1	NT	Anthonomus pomum period clock protein homolog mRNA, complete cds
3747	16348	288116		5.6	5.0E-02 U127689.2	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
5102	17874	30114		1.11	5.0E-02 AF188530.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6279	18837	31656		0.74	5.0E-02 AF086284.1	NT	Mus musculus Dmp-1 gene, exons 1-6
6450	19051			1.23	5.0E-02 AJ242825.1	NT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7544	20084	328338		10.74	5.0E-02 P35818	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fitsc) mRNA, complete cds
10101	22596	355598		1.13	5.0E-02 AF305238.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
11384	23816	38977		2.87	5.0E-02 U67680.1	NT	NO-ON-TRANSIENT A PROTEIN
11736	24924			7.22	5.0E-02 Q04047	SWISSPROT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
242	12901			23.23	4.9E-02 M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275848.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25529	3.62	4.9E-02	AF275848.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	16838	28414	1.58	4.9E-02	P54268	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYUSSIAN ATROPHY PROTEIN)
3628	16231		0.83	4.9E-02	AA168640.1	EST_HUMAN	zeta8e12.51 Stratogene hNT neuron (#857233) Homo sapiens cDNA clone IMAGE:632828 3' similar to Ali repetitive element/contains element MSR1 repetitive element contains Ali repetitive element/contains element MSR1 repetitive element
3651	16254	28728	0.91	4.9E-02	AA400914.1	EST_HUMAN	Zf78e03_51 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3651	16254	28727	0.91	4.9E-02	AA400914.1	EST_HUMAN	Zf78e03_51 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4986	17540	28982	1.59	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
4986	17540	28983	1.59	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
6372	17631	30345	0.61	4.9E-02	76822616	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5406	17804		0.91	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
5425	17882		0.98	4.9E-02	AE001774.1	NT	Thermotoga maritima section 88 of 138 of the complete genome
5437	17882	30398	1.03	4.9E-02	MB4063.1	NT	Brucella suis heat shock protein hsp70 (hsp70) gene, complete cds; heat shock protein hsp40 (hsp40) gene, complete cds
5573	18204	30054	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30055	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
6573	18204	30055	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7198	19727	32578	0.90	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21030		0.38	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8889	21228	34140	0.7	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10183	22888	35681	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36788	3.67	4.9E-02	AF006303.1	NT	Homo sapiens propro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	88223890	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12431	24573			2.82	4.9E-02	M18641	NT
13022	25487			1.15	4.8E-02	D16471.1	Human mRNA, Xq terminal portion
3523	13022	25487		1.87	4.8E-02	D16471.1	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14804	27459		1.98	4.8E-02	W51883.1	EST_HUMAN
3244	15858	28339		2.34	4.8E-02	X1714.1	Human mRNA, Xq terminal portion
4778	17359			1.32	4.8E-02	Z54280.1	Tetrahymanita rostrata histone H3II and Histone H4II Intergenic DNA
6309	17871	30233		0.67	4.8E-02	LS1914.1	S.sciro gene for skeletal muscle myodine receptor
5380	17839	30352		4.1	4.8E-02	AF189339.1	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
5380	17839	30353		4.1	4.8E-02	AF189339.1	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	20822	33535	1.42	4.8E-02	AW389497.1	EST_HUMAN	MR2-ST0129-221089-012-b02 ST0129 Homo sapiens cDNA
8087	21594	34824	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rp24 gene
8087	21594	34825	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rp24 gene
12018	24315		1.93	4.8E-02	98812893	NT	Streptococcus thermophilus bacteriophage Sfi 19, complete genome
8918	18577	32408	2.98	4.7E-02	W01153.1	EST_HUMAN	y20709_r1 Scores: melanocyte 2/NBHM Homo sapiens cDNA clone IMAGE:2810175 similar to contains: Alu repetitive element
8985	18542	32384	0.78	4.7E-02	BF689625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5
8985	18542	32395	0.78	4.7E-02	BF689625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5
8998	19498	32317	1.57	4.7E-02	M62752.1	EST_HUMAN	Rat statin-related protein (st1) gene, complete CDS
8193	20734	33844	8.55	4.7E-02	X15543.1	NT	B_taurus mRNA for RF-36-DNA-binding protein
8883	21421	34548	1.12	4.7E-02	X89221.1	NT	H_sapiens DNA for endogenous retroviral like element
8898	21444		2.28	4.7E-02	AB028678.1	NT	Catfish gillius Wpka-8 gene, complete cds
9154	21689	34633	6.91	4.7E-02	X15543.1	NT	B_taurus mRNA for RF-36-DNA-binding protein
8508	22026	35024	0.55	4.7E-02	BF305237.1	EST_HUMAN	6018926822F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5
8850	22149		0.55	4.7E-02	AB73042.1	EST_HUMAN	we70c10_x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3
10834	23189	38177	1.55	4.7E-02	67754585	NT	Mus musculus Igand of numb-protein X (lnd), mRNA
11430	23881	36945	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36946	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11851	25087		6.94	4.7E-02	AY648521	EST_HUMAN	AV648521 GLC_Homo sapiens cDNA clone GLCB2D022' 3'
12322	25089		1.47	4.7E-02	Ps2851	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
292	12948	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251189-003-905 HT0338 Homo sapiens cDNA
789	13388	25387	2.44	4.6E-02	AE00445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1335	13929		1.37	4.6E-02	AI014255.1	EST_HUMAN	am500d2.81 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:15388079 3' similar to TR:PF90533
1403	13996	28525	9	4.6E-02	AV7727059.1	EST_HUMAN	AV727658 HTC_Homo sapiens cDNA clone HTCBW001 5'
2530	15094	27088	2.77	4.6E-02	AW236023.1	EST_HUMAN	xn24103_x1 NCL_CGAP_Kdr11 Homo sapiens cDNA clone IMAGE:2894453 3' similar to SW:GRF1_HUMAN
2834	12948	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1:
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251189-003-905 HT0339 Homo sapiens cDNA
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251189-003-905 HT0339 Homo sapiens cDNA
4201	16780		0.97	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddz21) gene, complete cds
5809	18531	31256	1.44	4.6E-02	AF078892.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Grnh2)
6377	18981	31760	3.77	4.6E-02	X01624.1	NT	C_reinhardtii esp2 (espB) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18891	31761	3.77	4.6E-02	X61624.1	NT	C.leti ⁿ handtii shp2 (atypB) mRNA
68891	19825	32461	1.39	4.6E-02	A148574.1	EST_HUMAN	qe60b08.x11 Scores_pleacenta_8to9weeks_2NbHP80d9W Homo sapiens cDNA clone IMAGE:1713971 3'
88590	21129	34046	2.82	4.6E-02	BE154006.1	EST_HUMAN	similer to contains L1 L3 L1 repetitive element; PNO-HTC0339-080400-009-G12 HT0339 Homo sapiens cDNA
11281	23734	36789	4.28	4.6E-02	AA813928.1	EST_HUMAN	c277h09.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12541	24851		2.54	4.6E-02	X57803.1	NT	Human genuine immunoglobulin lambda light chain gene
472	13105	25598	2.71	4.5E-02	P22443	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1280	13857	26373	0.73	4.5E-02	AF005730.1	NT	Marburg Virus strain M/S.Africa/Johannesburg/1987/5/Ozdin VP35 gene, complete cds
1280	13857	26374	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1987/5/Ozdin VP35 gene, complete cds
1840	14428	26890	3.54	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2158	14733	27306	3.85	4.5E-02	AE003084.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3798	16346	28852	3.84	4.5E-02	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6378	18982	31762	1.88	4.5E-02	AJ40877.1	NT	Homo sapiens ASCL3 gene, CEEGP1 gene, C11orf16 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
6631	19227	32032	0.89	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8332	20873	33795	1.8	4.5E-02	AF036684.1	NT	Arribalzaga thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
88690	22357	35337	5.91	4.5E-02	AA325216.1	EST_HUMAN	EST28187 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10117	22812	35602	0.77	4.5E-02	AB004470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
11947	24276	31018	2.92	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFP-L3), mRNA
12367	24973	30838	6.27	4.5E-02	AA191087.1	EST_HUMAN	2043f11.r1 Striogene HNT neuron (#837223) Homo sapiens cDNA clone IMAGE:1832483 5'
237	12897		3.08	4.4E-02	BE97273.1	EST_HUMAN	1601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3905388 5'
2144	14772		0.8	4.4E-02	P31588	SWISSPROT	HYPOTHETICAL PROTEIN (ORF2280)
2532	15098	27688	2.62	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-072 P10012 Homo sapiens cDNA
3702	16303	28771	1.5	4.4E-02	AF156160.1	NT	Mycobacterium smegmatis Kinesse Pt10 (ptn10) gene, complete cds
4733	17314	29758	1.23	4.4E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4733	17314	29757	1.23	4.4E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32551	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7172	19704	32552	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8887	21228	34146	2.04	4.4E-02	AA736869.1	EST_HUMAN	rw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
10951	23488	36489	4.58	4.4E-02	AF080688.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11080	23592	36829	2.63	4.4E-02	AA498739.1	EST_HUMAN	as633f03.r1 Gossypier Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11684	24088			3.28	4.4E-02 AB040926.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
813	13431	25938	8.91	4.3E-02 AF003249.1	NT	Marine sponges myosin heavy chain FM3A (FM3A) mRNA, complete cds	
2803	15185	27732	1.16	4.3E-02 AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'	
2477	16883	26557	8.12	4.3E-02 AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
3720	16321			1.12	4.3E-02 AF069568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	19219	32023	5.71	4.3E-02 P30427	SWISSPROT	PLECTIN	
6822	19219	32024	5.71	4.3E-02 P30427	SWISSPROT	PLECTIN	
6830	19230	32239	0.68	4.3E-02 AA652268.1	EST_HUMAN	ns89c12-51 NCI CGAP_Pt2 Homo sapiens cDNA clone IMAGE:1188888	
8450	20890	33898	0.74	4.3E-02 AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced	
8738	21275	34198	0.98	4.3E-02 X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule	
8738	21275	34197	0.98	4.3E-02 X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule	
855	13471	25882	1.57	4.2E-02 AU12327.1	EST_HUMAN	AU12327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'	
889	13513		2.24	4.2E-02 AU12327.1	EST_HUMAN	AU12327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'	
829	13542	26080	0.89	4.2E-02 AW003845.1	EST_HUMAN	WA3407.1 NCI_CGAP_PtII Homo sapiens cDNA clone IMAGE:2545564 3' similar to TR:083291 Q83291 L1 RETROPOSON, ORF2 mRNA; contains L1.13 L1.1 repetitive element;	
1758	14348		1.32	4.2E-02 AL445068.1	NT	Thermoplasma acidophilum complete genome, segment 4/5	
3180	15802	28274	0.88	4.2E-02 AM83472.1	EST_HUMAN	Q19510.1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:NM35718	
3726	16327	28784	1.36	4.2E-02 P23091	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); TRANSFORMING PROTEIN MAP	
4410	168865	29437	1.03	4.2E-02 U28674.1	NT	Saccharomyces cerevisiae general sporulation (SSG1) gene, complete cds	
4410	168865	29438	1.03	4.2E-02 U28674.1	NT	Saccharomyces cerevisiae general sporulation (SSG1) gene, complete cds	
4854	17432	29883	0.69	4.2E-02 BF342885.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'	
5802	18427	31145	1.49	4.2E-02 AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds	
5802	18427	31146	1.49	4.2E-02 AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds	
7534	20054	32227	5.29	4.2E-02 AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds	
8745	21284	34206	3.5	4.2E-02 P05085	SWISSPROT	ALPHA-ACTinin 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)	
16069	22584	35559	1.17	4.2E-02 Q18850	SWISSPROT	T-BRAN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-50)	
10919	23438	36458	3.12	4.2E-02 AA976118.1	EST_HUMAN	an33b11.51 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558481 3' similar to gb:NM85280	
11187	23692	36739	2.3	4.2E-02 BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN); PM3-BN0174-255050-008-d10 BN0174 Homo sapiens cDNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11187	23692	36740	2.3	4.2E-02	BE816822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA, complete cds
11379	23831	36894	2.06	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
122226	25023		3.4	4.2E-02	AI883494.1	EST_HUMAN	wksg10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
5336	13167	25948	0.7	4.1E-02	AF200029.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15258	27828	2.87	4.1E-02	AE002230.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4571	17154		8.95	4.1E-02	AW883484.1	EST_HUMAN	QV1-NN0012-180403-164-008 NN0012 Homo sapiens cDNA
5295	17957		0.69	4.1E-02	X85880.1	NT	Lymphocyte genes type 3 partial lyp gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE261894.1	EST_HUMAN	601107535F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856 5
5824	18448	31171	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856 5
68922	19539		0.97	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7158	19588	32632	1.92	4.1E-02	AE0022132.1	NT	Ureaplasma urealyticum section 33 of 58 of the complete genome
75222	20342	32911	1.76	4.1E-02	7862247	NT	Homo sapiens KIAA0887 protein (KIAA0887). mRNA
7742	20250	33143	3.14	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8577	21119	34030	0.93	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9081	21617	34552	0.85	4.1E-02	AA372398.1	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	
12572	25024	30618	24.9	4.1E-02	AJ271900.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3261	15892	28371	3.71	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
38688	16495	28928	0.98	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
52385	17858	30284	0.58	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltryptophylpeptidyl synthetase, complete cds
5581	18212	30881	5.51	4.0E-02	AF280107.1	NT	4(CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6332	18988	31744	1.65	4.0E-02	BF10434.1	EST_HUMAN	7n52107.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:35688380 3' similar to TR:0752288 O752288
7678	20169	33078	6.8	4.0E-02	L28838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8851	21190	34108	2.84	4.0E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9562	22062		0.84	4.0E-02	BF078376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
8586	22088	35051	3.35	4.0E-02	AJ00941.1	NT	Methanobacterium thermophilicum strain Marburg, Thiofumarate reductase subunit A

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8895 22892			1.28	4.0E-02	D43948_1	NT	Human mRNA for KIAA0082 gene, partial cds
116088 24651			1.62	4.0E-02	AJ001018_1	NT	Kluveromyces lactis gene for Cet-A+ ATPase
116841 24634	30788		18.69	4.0E-02	AJ001058_1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1159 13702	28273		3.8	3.9E-02	BF510149_1	EST_HUMAN	UH-BW_1-est-h-08-0-U.1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
13890 13894	28510		1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004 14688	27145		2.67	3.9E-02	AJ403388_1	NT	M.musculus DNA for desmin-binding fragment DesD7
27228 15283			1.85	3.9E-02	45068862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
53225 17887	30303		0.6	3.9E-02	AW382417_1	EST_HUMAN	RC8-ST0258-171186-021-C08 S70258 Homo sapiens cDNA
5344 17805	30320		1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5344 17805	30321		1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
56887 18213	30810		0.73	3.9E-02	D50808_1	NT	Rat gene for cholecytokinin type-A receptor (CCKAR), complete cds
56887 18213	30811		0.73	3.9E-02	D50808_1	NT	Rat gene for cholecytokinin type-A receptor (CCKAR), complete cds
56906 18258	31254		1.24	3.9E-02	BE98841_1	EST_HUMAN	601648374F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3853842 5'
60118 18837	31377		0.68	3.9E-02	BF875203_1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7118 19458	32273		1.01	3.9E-02	BE271437_1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7781 20324	33223		0.93	3.9E-02	BF238613_1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8004 20548	33449		0.56	3.9E-02	AJ226041_1	NT	Homo sapiens 959 kb contig between AM.1 and CBR.1 on chromosome 21q22; segment 1/3
8004 20548	33450		0.56	3.9E-02	AJ226041_1	NT	Homo sapiens 959 kb contig between AM.1 and CBR.1 on chromosome 21q22; segment 1/3
11287 20288	33188		1.6	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11691 24981			7.19	3.9E-02	AB042563_1	NT	Falls cathe G-CSF gene for granulocyte-stimulating factor, complete cds
12373 24543			1.73	3.9E-02	U68061_1	NT	
12503 24602			64.84	3.9E-02	AL049866_2	NT	
1985 14577	27137		1.24	3.9E-02	BE885137_1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
4887 17571	30015		0.89	3.8E-02	BE38275_1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3828757 5'
4887 17571	30016		0.99	3.8E-02	BE38275_1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3828757 5'
5062 17635	30078		0.93	3.8E-02	AU124122_1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001688 5'
56832 18281	30733		1.19	3.8E-02	M11228_1	NT	Human protein C gene, complete cds
6237 18848	31617		1.07	3.8E-02	P10284	SWISSPROT	HOMEBOX PROTEIN HOXA-4 (HOX-2.6)
7359 18885	32748		1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member B (ABCA8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	21137			1.3	3.8E-02 M80875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10506	23000			0.47	3.8E-02 AE001328.1	NT	Chlamydia trachomatis section 58 of 87 of the complete genome
10532	23059	36082		2.17	3.8E-02 AF143982.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1029	13639	26154		3.69	3.7E-02 P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26593		1.15	3.7E-02 L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430		4.49	3.7E-02 A1894806.1	EST_HUMAN	nr85081x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502.3'
2813	15175	27743		0.83	3.7E-02 AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3088	15701	28174		0.97	3.7E-02 P78844	SWISSPROT	EOMESODERMIN
3088	15703	28175		4.74	3.7E-02 BF312803.1	EST_HUMAN	601689823F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584.5'
7138	25118			0.73	3.7E-02 AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
8628	22424			0.89	3.7E-02 AA782516.1	EST_HUMAN	nr5509.61 Scores_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone 1360912.3'
11735	24139	37158		7.89	3.7E-02 BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973.5'
12435	24868	30707		3.02	3.7E-02 11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784		0.82	3.6E-02 X73221.1	NT	H. vulgaris Ss1 gene for sucrose synthase
3723	16324	28701		0.87	3.6E-02 AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q28.3] of Homo sapiens
5620	18248	30701		0.77	3.6E-02 X56403.1	NT	C. glutamicum gsp, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717		0.77	3.6E-02 X56403.1	NT	C. glutamicum gsp, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
6808	19389	32213		5.32	3.6E-02 AW845516.1	EST_HUMAN	CM2-EN0013-110500-192-610 EN0013 Homo sapiens cDNA
6808	19399	32214		5.32	3.6E-02 AW845516.1	EST_HUMAN	CM2-EN0013-110500-192-610 EN0013 Homo sapiens cDNA
7143	19878	32616		1.68	3.6E-02 AF025952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
7347	19873	32739		3.52	3.6E-02 AA714521.1	EST_HUMAN	nrw2005.51 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024.3' similar to gb:J00314_ma2
7629	20141	33020		0.88	3.6E-02 BE145078.1	EST_HUMAN	MR0-H70158-030200-023-508 HT0158 Homo sapiens cDNA
8313	21827	34776		1.87	3.6E-02 U20808.1	NT	Dicyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9313	21827	34777		1.87	3.6E-02 U20808.1	NT	Dicyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34989		0.72	3.6E-02 BF347598.1	EST_HUMAN	602020453F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153116.5'
9228	19341	26059		1.57	3.5E-02 U098506.1	NT	Drosophila melanogaster ligerin mRNA, complete cds
1046	13654	26163		2.28	3.5E-02 AF253417.1	NT	Homo sapiens microsome epsilon hydrolase (EPHX1) gene, complete cds

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1610	14203	28739	1.49	3.5E-02	BF878085.1	EST_HUMAN	6020851_38F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:42483775'
1610	14203	28737	1.49	3.5E-02	BF878085.1	EST_HUMAN	6020851_38F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:42483775'
4283	16879	28326	1.91	3.5E-02	AE001773.1	NT	Thermatoga maritime section 85 of 138 of the complete genome
4406	16891	28435	1.16	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	16874	31752	2.11	3.5E-02	J01288.1	NT	Maize eth1 gene (Mac1), complete cds
7918	20490		0.82	3.5E-02	H28851.1	EST_HUMAN	yp44605J1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:1902586 5' similar to contains Ali repetitive element.
85558	21097	34018	3.5	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:39287373'
8831	22427	35401	2.44	3.5E-02	X78842.1	NT	Lascis MA31363 gtpE and dnk genes
8977	22472	35455	0.49	3.5E-02	BE581042.1	EST_HUMAN	601344861F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:38777654_5'
11297	23819	36880	1.92	3.5E-02	AW801641.1	EST_HUMAN	PM1-CT0328-281288-0024-R03 CT0328 Homo sapiens cDNA
11387	23619	36881	1.92	3.5E-02	AW801641.1	EST_HUMAN	PM1-CT0328-281288-0024-R03 CT0328 Homo sapiens cDNA
12257	24534		1.39	3.5E-02	AF009883.1	NT	Homo sapiens T cell receptor beta locus, TCRBV21S2A2 region
12429	24913		4.38	3.5E-02	BE2708948.1	EST_HUMAN	601178785F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833_5'
604	13223	25708	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ20013 protein, partial cds
604	13223	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ20013 protein, partial cds
605	13223	25708	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ20013 protein, partial cds
605	13223	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ20013 protein, partial cds
1089	13694	26203	3.22	3.4E-02	AW274020.1	EST_HUMAN	SW:C211_HUMAN_P3801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR :
1248	13845		6.54	3.4E-02	11345459	NT	yc20e03.11 Soares lung (#307210) Homo sapiens cDNA clone IMAGE:811260 5' similar to contains MER20 repetitive element
2435	15002	27574	1.82	3.4E-02	T57180.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3478	16084	28558	1.11	3.4E-02	AL163208.2	NT	RC3-FN0155-060700-011-d10 Fl0155 Homo sapiens cDNA
3843	16442	28603	0.68	3.4E-02	BE838514.1	EST_HUMAN	RC8-LM0015-210200-021-A10 UM0015 Homo sapiens cDNA
3863	16591	28663	4.29	3.4E-02	AW704052.1	EST_HUMAN	M.musculus S-antigen gene promoter region
4703	17285	28730	3.17	3.4E-02	X59798.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5217	17782		2.61	3.4E-02	O28457	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
5237	17801	30220	1.47	3.4E-02	AJ012469.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4032434_5'
6353	18658		0.68	3.4E-02	BF131628.1	NT	Human lysyl adductase-like protein gene, exon 3
6658	18046	30468	4.63	3.4E-02	U24393.1	NT	wi89d4.1x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:24533031_3
8204	20745		3.76	3.4E-02	AI888829.1	EST_HUMAN	wi89d4.1x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:24533031_3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8882	21221	34141	1.64	3.4E-02	AA684686.1	EST_HUMAN	nu70708.3 NCI_CGAP_AV1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element;contains element MER25 MER25 repetitive element;
8848	21397			5.71	3.4E-02	AA194308.1	Zg04f11.3 Stratagene muscle S37/209 Homo sapiens cDNA clone IMAGE:628749 3' similar to
8893	22192			0.53	3.4E-02	AB092719.1	TR:G1017425 G1017425
3865	13041			11.74	3.3E-02	AA398735.1	IPISGKPLPKVTLSRDGVPLKA TMRFNTTEAENL TNLKESVTADAGRYEITAANSSGGTAKAFINIVLDRPG
12098	13898	28322		18.12	3.3E-02	AB035887.1	PPT GPVISDTEEVTLKWEPPKYDGGSQVNTNYILLKRETSTAVNTEVSA TVARTMMKVMKL ...;
1681	14273	28908		1.20	3.3E-02	AF110763.1	0286h108.x1 Scores_perathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1683519 3'
1775	14335			1.28	3.3E-02	AE000700.1	Z75e08.81 Scores_basis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
2131	14706			2.05	3.3E-02	R08112.1	Chirostoma girela CYP2A17 mRNA for cytochrome P450 2A17, complete cds
3406	16015	28484		0.85	3.3E-02	H02389.1	NT
4259	14273	28908		2.91	3.3E-02	AF110763.1	NT
4586	17149	28598		2.15	3.3E-02	6755882	NT
6561	19159	31958		28.84	3.3E-02	BF245895.1	NT
6561	18169	31657		23.84	3.3E-02	BF245895.1	EST_HUMAN
8249	21772	34721		0.73	3.3E-02	BF115621.1	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8248	21772	34722		0.73	3.3E-02	BF115621.1	Mus musculus tumor rejection antigen gp98 (Trat1), mRNA
8345	21858	34807	0.59	3.3E-02	AA488202.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8345	21859	34808	0.58	3.3E-02	AA488202.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
10491	23885		0.5	3.3E-02	H38109.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
11000	23514	30548	3.5	3.3E-02	BF691107.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
11832	24288		2.14	3.3E-02	T088545.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
12089	24358		2.06	3.3E-02	W61860.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
137	12802	25291	1.87	3.2E-02	AJ022005.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
1165	13767	28277	18.04	3.2E-02	AF086275.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
1165	13767	28278	19.04	3.2E-02	AF086275.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
1808	14398	28943	1.38	3.2E-02	AF128894.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
2164	14141		1.35	3.2E-02	P28855	SWISSPROT	LARGE EGUMENT PROTEIN
2885	12802	25281	0.59	3.2E-02	AJ022005.1	EST_HUMAN	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3168	15782	28253	12.01	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849727 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3778	16378	28842	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4299	16895		20.05	3.2E-02	X94788.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4882	17457	28809	3.35	3.2E-02	AF114182.1	NT	Saxatilagia nitifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5728	18352	31055	1.45	3.2E-02	X68709.1	NT	S.griseocarnineum whtG-SIV gene
5728	18352	31058	1.45	3.2E-02	X68709.1	NT	S.griseocarnineum whtG-SIV gene
6646	18242	32045	2.59	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98-14
6847	19243		27.51	3.2E-02	T88367.1	EST_HUMAN	Alu repetitive element; contains L TR1 repetitive element;
6722	18316	32119	3.78	3.2E-02	AF173845.1	NT	Segulus oedipus tissue kalikrein gene, complete cds
7739	20247	33140	0.85	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily IIIB (phenobarbital-inducible) (CYP2B), mRNA
8242	20783	33702	13.00	3.2E-02	6690585	NT	Mus musculus kinetin family member 3c (Kif5c), mRNA
8871	21410		0.69	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34630	1.08	3.2E-02	AI278971.1	EST_HUMAN	qm1704.X1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882003 3'
9152	21687	34631	1.00	3.2E-02	AI278971.1	EST_HUMAN	qm1704.X1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882003 3'
8869	22484		4.05	3.2E-02	AA710795.1	EST_HUMAN	255Ab12.51 Soares pined gland N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to dd1L0841 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10280	22765	35743	0.95	3.2E-02	UB67162.1	NT	Macaca mulatta cholinergic receptor CCR5 mRNA, complete cds
1303	13687		1.8	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1348	13943	26486	1.28	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1838	14520	27076	1.52	3.1E-02	68711584	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
2017	14569		1.14	3.1E-02	250097.1	NT	Drosophila melanogaster mRNA for headcase protein
5207	17772		0.87	3.1E-02	BE091889.1	EST_HUMAN	IL2-BT0733-130400-067-A06 B10733 Homo sapiens cDNA
5331	17892		3.08	3.1E-02	AL161550.2	NT	Anabidopsisthaliana DNA chromosome 4, contig fragment No. 50
5371	18918		0.58	3.1E-02	AU116008	EST_HUMAN	AU116008 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5468	18102	30421	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5563	18194		2.32	3.1E-02	AA278478.1	EST_HUMAN	Zs81a06.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703898 5'
5829	18453	31178	0.8	3.1E-02	BFR87742.1	EST_HUMAN	602098783F1 NIH MGIC_57 Homo sapiens cDNA clone IMAGE:4086709 5'
8844	22439	35417	3.63	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
12667	24737		2.24	3.1E-02	AW488414.1	EST_HUMAN	he3707.X1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2821221 3'
1684	14257		2.3	3.0E-02	AF187125.1	NT	Phytoketones minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2821	15183	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	265h03.11 Soares_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3823	16226	28704	1.24	3.0E-02	M94178.1	NT	Seccheromyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3714	16316	28783	3.07	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II amidotransferase gene, complete cds
3808	18407		0.78	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-009 ST0286 Homo sapiens cDNA 5' end
4021	16819		0.74	3.0E-02	AA384003.1	EST_HUMAN	EST74530 Pitressin gland II Homo sapiens cDNA 5' end
5000	17573	300117	1.04	3.0E-02	BE782830.1	EST_HUMAN	60147231F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3876503 5'
5208	17773	301195	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	301196	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17885	30289	1.1	3.0E-02	BE968917.1	EST_HUMAN	601649872F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:38333828 3'
5590	18221		3.62	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6402	19006	31784	0.78	3.0E-02	N88915.1	EST_HUMAN	zcs8e10.1 Scans fetal liver splean INF1S Homo sapiens cDNA clone IMAGE:284908 5' similar to contains zcs8e10.1 Scans fetal liver splean INF1S Homo sapiens cDNA clone IMAGE:284908 5' similar to contains element TAR1 repetitive element;
6402	19005	31785	0.78	3.0E-02	N88915.1	EST_HUMAN	element TAR1 repetitive element;
6402	19005	32045	2.83	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6884	19619	32453	3.15	3.0E-02	BE88948.1	EST_HUMAN	6015122D8F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3813848 5'
6887	19485	32209	3.15	3.0E-02	BE88948.1	EST_HUMAN	6015122D8F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3813848 5'
6887	19485	32207	3.15	3.0E-02	BE88948.1	EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
7131	19471	32280	1.83	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
7131	19471	32281	1.83	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
7252	18810	32888	1.92	3.0E-02	M88624.1	NT	Human dystrophin gene
7583	20088		0.78	3.0E-02	BIF246361.1	EST_HUMAN	601854887F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8575	21114	34033	0.78	3.0E-02	BFS53889.1	EST_HUMAN	IL6-HT0704-280800-008-004 HT0704 Homo sapiens cDNA
8728	21287		1.77	3.0E-02	AF275854.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	22851	35945	1.49	3.0E-02	AE001787.1	NT	Thermitoga maritima section 109 of 139 of the complete genome
10441	22835	35944	0.46	3.0E-02	Z2121.1	EST_HUMAN	HSAAUDITH TEST1. Human adult Testis tissue Homo sapiens cDNA clone IMAGE:244 (b)
11111	23821	36882	4.11	3.0E-02	MB1357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11539	23988	37057	8.47	3.0E-02	AA48216.1	EST_HUMAN	ns8704.81 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283
12043	25078	30515	2.58	3.0E-02	R32019.1	EST_HUMAN	yf63d04.81 Scans placenta Nb2kIP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24570		18.42	3.0E-02	AW889595.1	EST_HUMAN	QV4-NR0038-270400-187-405 NR0038 Homo sapiens cDNA
12460	25069		3.53	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2478	15487	27814	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE585644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680685 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15637	28115	1.11	2.9E-02	BE585844.1	EST_HUMAN	601338428F1 NIH MGC_53 Homo sapiens cDNA clone IMAGE:3880895 5'
3616	16219	288988	0.84	2.9E-02	X55264.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	28075	0.68	2.9E-02	H72805.1	EST_HUMAN	y07610.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18018	6236	2.9E-02	R09121.1	EST_HUMAN	Y25c09.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'	
6213	18823	31594	1.31	2.9E-02	AF080221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	18037	31824	6.5	2.9E-02	BF032238.1	EST_HUMAN	601452881F1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3856698 5'
7286	18824	32883	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5'
7455	18878	32845	0.67	2.9E-02	D28241.1	EST_HUMAN	HUMN022 Human epidermal keratinocyte Homo sapiens cDNA clone 262
7840	20482	33393	0.91	2.8E-02	AF123278.1	NT	Buchnera aphidicola natural-host Schlechtedella chinensis gluconate-β-phosphate dehydrogenase (grd) gene, partial cds
7940	20482	33394	0.91	2.8E-02	AF123278.1	NT	Buchnera aphidicola natural-host Schlechtedella chinensis gluconate-β-phosphate dehydrogenase (grd) gene, partial cds
8577	22077	35040	2.16	2.8E-02	AW875978.1	EST_HUMAN	CN3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
8577	22077	35041	2.16	2.8E-02	AW875978.1	EST_HUMAN	CN3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9788	22288		0.59	2.8E-02	AW976597.1	EST_HUMAN	EST388708 MAGE gene sequences, MAGN Homo sapiens cDNA Aeropyrum pernix genomic DNA, section 7/7
10247	22742	35732	0.94	2.8E-02	AP080084.1	NT	Sheep gene for ultra high-sulphur keratin protein
10625	16219	28898	1.73	2.8E-02	X55294.1	NT	AU135617 PLACE1 Homo sapiens cDNA clone PLACE1002892 5'
12045	24979		1.88	2.8E-02	AU135817.1	EST_HUMAN	EST382234 MAGE gene sequences, MAGK Homo sapiens cDNA
561	13221		0.98	2.8E-02	AW970153.1	EST_HUMAN	Homo sapiens retinal fission (FSCN2) gene, exon 2
3414	16022	28502	1.62	2.8E-02	AF068063.1	NT	Homo sapiens retinal fission (FSCN2) gene, exon 2
3414	16022	28503	1.62	2.8E-02	AF068063.1	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
4401	16986		0.71	2.8E-02	83893751	NT	L208SF Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L20833 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE
5337	17889	34913	0.92	2.8E-02	NB70773.1	EST_HUMAN	6015844078F1 NIH MGC_9 Homo sapiens cDNA clone IMAGE:39480867 5'
5679	18306	30802	11.28	2.8E-02	BE741083.1	EST_HUMAN	y221b08.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1088355 5'
6900	19634	32472	1.14	2.8E-02	T78980.1	NT	Craterostigma planlagaeum mRNA for homeodomain leucine zipper protein (hb-1)
8270	20811	33732	1.8	2.8E-02	AJ005820.1	EST_HUMAN	2s8cc08.71 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:711466 5'
8847	21485	34407	0.74	2.8E-02	AA290782.1	EST_HUMAN	Canis porcellus inward-rectifying potassium channel K12.1 (KCNJ2) gene, complete cds
9135	21670	34612	0.91	2.8E-02	AF187872.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9237	21763	34709	0.84	2.8E-02	AE001092.1	EST_HUMAN	6012039477F2 NCI CGAP Brm67 Homo sapiens cDNA clone IMAGE:4177287 5'
10498	22892	36002	1.81	2.8E-02	BFS27244.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
3478	19085	28559	4.18	2.7E-02	AI191484.2	EST_HUMAN	yy88n12.11 Soares multiple sclerosis cDNA clone IMAGE:2804487 5'
4280	16986	28312	1.81	2.7E-02	N47258.1	EST_HUMAN	yy88n12.11 Soares multiple sclerosis cDNA clone IMAGE:2804487 5'
4280	16986	28313	1.81	2.7E-02	N47258.1	EST_HUMAN	yy88n12.11 Soares multiple sclerosis cDNA clone IMAGE:2804487 5'

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Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
56833	18282	30734	1.11	2.7E-02 R12245.1	EST_HUMAN	y33d99_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128857 5' similar to SP:JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6081	18678	31420	0.7	2.7E-02 X61870.1	NT	T-bestium PTTH20 mRNA for wheat type V thiamin
6713	18307		0.9	2.7E-02 X97580.1	NT	A.Bisporus pgA gene
7127	19487	32285	2.08	2.7E-02 AA983571.1	EST_HUMAN	o886103_s1 Soares_total_fetus_Nb25IF8_9v Homo sapiens cDNA clone IMAGE:1624661 3'
8295	20836		1.21	2.7E-02 A1377038.1	EST_HUMAN	tc28q08_x1 Soares_total_fetus_Nb25IF8_9v Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element
597	13268	25700	1.52	2.6E-02 AL1632822.2	NT	Homo sapiens chromosome 21 segment HS21C082
2404	14972	27644	2.78	2.6E-02 AAA90021.1	EST_HUMAN	ab026c02_s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:8395985 3'
2408	14974	27548	7.53	2.6E-02 8754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2408	14974	27547	7.53	2.6E-02 8754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2840	15556		1.17	2.6E-02 AF108908.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G8, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5031	17605	30049	4.74	2.6E-02 L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
6224	17789	30298	1.58	2.6E-02 AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 239 of the complete chromosome 1
5254	17817	30241	2.94	2.6E-02 AW241154.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0068 ;
6338	18972		6.32	2.6E-02 A1209030.1	EST_HUMAN	q927f11_x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6559	19154	31980	2.29	2.6E-02 BE621748.1	EST_HUMAN	60148347311 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6815	19574	32422	0.75	2.6E-02 Z989084.1	NT	Vaccinia virus ORF11, strain Wyeth
6915	19574	32463	0.75	2.6E-02 Z989084.1	NT	Vaccinia virus ORF11, strain Wyeth
6890	19489	32310	8.45	2.6E-02 6881271	NT	Rattus norvegicus Neve growth factor receptor, fast (Ngfr), mRNA
8442	20982	33897	0.77	2.6E-02 AA868048.1	EST_HUMAN	ak2ZD14_s1 Soares tests NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9282	21882	34827	1.41	2.6E-02 11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9830	22130	35094	0.8	2.6E-02 AF114852.1	NT	Saccharomyces cerevisiae NRFL_Y-126339(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
9830	22130	35095	0.6	2.6E-02 AF114852.1	NT	encoding mitochondrial protein, complete cds
10302	22798	35787	4.1	2.6E-02 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11265	23783		2.44	2.6E-02 AA279351.1	EST_HUMAN	z884cd271 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11437	23887		1.63	2.6E-02 AW500547.1	EST_HUMAN	UHF-BN-ah-104-U1.H NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3017448 5'
11985	25060	30512	1.28	2.6E-02 BF349827.1	EST_HUMAN	602016501F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150944 5'
12083	24354		1.29	2.6E-02 11422836	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
557	13188	25688	1.78	2.6E-02 AI793130.1	EST_HUMAN	an26108_s5 NCI CGAP_Lus Homo sapiens cDNA clone IMAGE:1567827 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
557	13188	25887		1.78	2.6E-02 A1783130.1	EST_HUMAN	an28076.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'	
842	13458	25987	19.68	2.5E-02 BE974314.1	EST_HUMAN	801680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'		
802	13516	26034	4.48	2.5E-02 BE974314.1	EST_HUMAN	801680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'		
2781	15344			2.84	2.6E-02 U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds	
2983	15599	26078	3.52	2.5E-02 X89887.1	NT	H.cartier mRNA for fucoxanthin chlorophyll a/b binding protein, Fcp1		
2983	15599	26079	3.52	2.5E-02 X89887.1	NT	H.cartier mRNA for fucoxanthin chlorophyll a/b binding protein, Fcp1		
4119	18005	28167	0.77	2.6E-02 BE701165.1	EST_HUMAN	PM2-NM0128-080700-001-a12 NR0128 Homo sapiens cDNA		
4119	18005	28168	0.77	2.5E-02 BE701165.1	EST_HUMAN	PM2-NM0128-080700-001-a12 NR0128 Homo sapiens cDNA		
4284	16870	28318	5.25	2.5E-02 AW582114.1	EST_HUMAN	h36f098.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'		
59889	18512	31238	0.7	2.6E-02 A1732778.1	EST_HUMAN	Z633C10J5 Scores_ovary tumor NBTIOT Homo sapiens cDNA clone IMAGE:810354 3'		
6340	18943			4.9	2.5E-02 BE670128.1	EST_HUMAN	7e20e00.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1,L1,L1	
6357	18981			4.3	2.5E-02 BE748898.1	EST_HUMAN	repetitive element;	
6478	19079	31982	0.72	2.5E-02 28029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds		
7680	20172	33058	1.52	2.5E-02 BF528722.1	EST_HUMAN	6020705622F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213408 5'		
7680	20172	33059	1.52	2.5E-02 BF528722.1	EST_HUMAN	6020705622F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213408 5'		
7820	20462	33988	0.48	2.6E-02 BE252489.1	EST_HUMAN	601108281F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'		
8759	21288	34219	0.93	2.5E-02 Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)		
8864	21432	34255	0.45	2.5E-02 AW028821.1	EST_HUMAN	wu03c10.x1 NCI_CG8 Homo sapiens cDNA clone IMAGE:2516370 3'		
8878	22473			0.8	2.5E-02 X71303.1	NT	D.radiata 2S ribosomal RNA, D2 domain	
10475	22869	35978	0.73	2.5E-02 AI147815.1	EST_HUMAN	gb2208.x1 Scores_pregnant uterus_NHPU_Homo sapiens cDNA clone IMAGE:16868982 3'		
10689	23219	36231	2.04	2.5E-02 Q10335	SWISSPROT	HYPOTHETICAL_46.7 KD PROTEIN C18G10.05 IN CHROMOSOME 1		
10689	23219	36232	2.04	2.5E-02 Q10335	SWISSPROT	HYPOTHETICAL_46.7 KD PROTEIN C18G10.05 IN CHROMOSOME 1		
10761	23285			4.04	2.5E-02 AF050157.1	NT	Mus musculus major histocompatibility protein class II alpha chain (Ia/alpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-2>	
11602	24043			1.73	2.5E-02 AB007548.1	NT	Homologous gene for LECT2, complete cds	
11922	24983			3.33	2.5E-02 11420078	NT	Home sapiens similar to ALEX3 protein (H. sapiens) (LOC36384), mRNA	
12115	24855			1.53	2.5E-02 11433220	NT	Home sapiens nitrogen-activated protein kinase kinase NckA (NckA) gene, complete cds	
12213	24438			2.17	2.5E-02 US0168.1	NT	Dictyostelium discoideum putative protein kinase NckA (NckA) gene, complete cds	
12242	24454	30957	1.31	2.5E-02 BE973327.1	EST_HUMAN	601682268R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:38955613 3'		
185	12846	25322	0.75	2.4E-02 A1375882.1	EST_HUMAN	tg72007.x1 Scores_fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:2070158 3'		
1642	14234	26768	2.09	2.4E-02 H65884.1	EST_HUMAN	y75f11.J1 Scores_fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:211149 5'		
2088	15457	27238	2.02	2.4E-02 P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))		

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02 P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))	
4459	17044	29487	1.89	2.4E-02 J05110.1	NT	T.thermophilus calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds	
4819	17202	28850	1.63	2.4E-02 P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))	
4819	17202	28851	1.63	2.4E-02 P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))	
6333	18987	31745	0.94	2.4E-02 W86880.1	EST_HUMAN	2h63h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'	
7273	19801	32658	1.06	2.4E-02 Z20573.1	EST_HUMAN	HSAAACCKXT_Human adult Rhinoblastoma cell-line Homo sapiens cDNA	
7287	19815	32672	0.95	2.4E-02 X12925.1	EST_HUMAN	Fat gene for uncoupling protein (UCP)	
7287	19816	32673	0.95	2.4E-02 X12925.1	EST_HUMAN	Fat gene for uncoupling protein (UCP)	
7831	20373	0.69	2.4E-02 AW813007.1	EST_HUMAN	RC3-ST0188-230300-019-h08 ST0188_Homo sapiens cDNA		
7884	20426		0.6	2.4E-02 M16780.1	EST_HUMAN	Human retrotransposon 3' long terminal repeat	
8379	20919		0.88	2.4E-02 HT78376.1	EST_HUMAN	YU12c05.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element contains A3R repetitive element;	
8488	21008	33925	< 10.74	2.4E-02 N89442.1	EST_HUMAN	ZB35g11.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:204586 3' similar to gbk[K02989]RATSRT7K_Rat (rRNA) contains A3R,b1 A3R repetitive element;	
8917	21455	34375	0.64	2.4E-02 AE001125.1	EST_HUMAN	Barrelia burgdorferi (section 11 of 70) of the complete genome	
8939	21477	34398	0.75	2.4E-02 AA825880.1	EST_HUMAN	ZU61c06.s1 Soares_fetus_NHT_Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN);contains Alu repetitive element contains element XTR repetitive element;	
9720	22218	35193	2.78	2.4E-02 AV882854.1	EST_HUMAN	AV682854 GKC_Homo sapiens cDNA clone GKCD8C003 5'	
9891	22388	36398	2.9	2.4E-02 AA482894.1	EST_HUMAN	MT07b12.s1 NCI_CQAP_Thy1_Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element contains element PTR5 repetitive element;	
11447	23897	36862	1.9	2.4E-02 AF108905.1	EST_HUMAN	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes	
11447	23897	36983	1.9	2.4E-02 AF108905.1	EST_HUMAN	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes	
11718	24127		3.56	2.4E-02 9627809	NT	Bacteriophage bl67, complete genome	
11868	24222	31044	2.48	2.4E-02 6753635	NT	Mus musculus Dm-B homolog 1 (E. coli) (DmB1), mRNA	
11924	24259	31013	1.36	2.4E-02 BE828898.1	EST_HUMAN	MRO-FT0175-310800-202-s08 FT0175_Homo sapiens cDNA	
11984	24294	30981			NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	
11984	24294	31025	1.38	2.4E-02 U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds							
12164	24404		8.87	2.4E-02	AB008569.1	NT	
12181	24422		2.11	2.4E-02	NA280.1	EST_HUMAN	Y08498.1 Soares melanocyte 2NIbHM Homo sapiens cDNA clone IMAGE:270610 5'
12187	24425		1.55	2.4E-02	BF870477.1	EST_HUMAN	602153281F1 NIH MGC_83 Homo sapiens cDNA clone IMAGE:4284173 5'
12382	24827	30785	1.48	2.4E-02	AA172683.1	EST_HUMAN	ZP13H01.1 Stratagene fetal retina 83/7202 Homo sapiens cDNA clone IMAGE:308981 5'
1813	14498		5.46	2.3E-02	W05340.1	EST_HUMAN	ZS8498.1 Soares fetal lung, NHL19N Homo sapiens cDNA clone IMAGE:288284 5'
1881	14515		21.88	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2053	14634	27205	0.80	2.3E-02	AW797355.1	EST_HUMAN	CM2-LN-W0038-280400-172-b11 UMM038 Homo sapiens cDNA
23889	14867	27529	2.31	2.3E-02	Z74263.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
9745	16346	28814	6.21	2.3E-02	Z20377.1	EST_HUMAN	HSAAAACDH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3777	16377		0.82	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (L GAL S3) mRNA, 3' end
4230	16818	28268	0.75	2.3E-02	L24799.1	NT	Gelius gelius connectin 45.8 (Cx45.8) gene, complete cds
4230	16818	29287	0.75	2.3E-02	L24790.1	NT	Gelius gelius connectin 45.8 (Cx45.8) gene, complete cds
4511	17085	28642	1.21	2.3E-02	AW869107.1	EST_HUMAN	CMA-NH0080-280400-160-b04 NMC080 Homo sapiens cDNA
4548	17130	28574	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-p07 MT0118 Homo sapiens cDNA
4548	17130	28676	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-p07 MT0118 Homo sapiens cDNA
4547	18008	28578	1.05	2.3E-02	AW683683.1	EST_HUMAN	X825d083.X1 NCI_CGAP_U12 NIH MGC_2770871 3'
4547	18008	28577	1.05	2.3E-02	AW583683.1	EST_HUMAN	X825d083.X1 NCI_CGAP_U12 NIH MGC_2770871 3'
4698	17280	29728	2.98	2.3E-02	BF028487.1	EST_HUMAN	60167278F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:39565388 5'
4698	17280	29727	2.98	2.3E-02	BF028487.1	EST_HUMAN	60167278F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:39565388 5'
5182	17748	30177	0.83	2.3E-02	AW844307.1	EST_HUMAN	RC2-QN0051-28010-011-a07 CN0051 Homo sapiens cDNA
5368	17928	30342	2.72	2.3E-02	AI038078.1	EST_HUMAN	alpha2C10.x1 Soares_fetal_liver_spleen_1NFLS_S1_Homo_sapiens_cDNA_clone IMAGE:1656978 3' similar to gb:X68608_mef1 ATP SYNTHASE LIPOID-BINDING PROTEIN P2 PRECURSOR (HUMAN); Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propanoyl-CoA carboxylase beta chain (pcB) homolog gene, partial cds
5578	18209	30659	3.34	2.3E-02	U80303.1	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 17
6773	19327	32132	4.43	2.3E-02	AL161505.2	NT	M00-HT0080-011088-002-c08 HT0080 Homo sapiens cDNA
7056	18075	30428	0.88	2.3E-02	BE141475.1	EST_HUMAN	Human plecan (PLEC1) gene, exons 3-32, and complete cds
7817	20360	33268	8	2.3E-02	U63610.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8407	20947	33387	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8407	20947	33368	0.74	2.3E-02	AJ298106.1	EST_HUMAN	WA76H10.x1 Soares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2302147 3'
8630	21169	34085	0.83	2.3E-02	AI685380.1	EST_HUMAN	WA76H10.x1 Soares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2302147 3'
8630	21169	34086	0.83	2.3E-02	AI685380.1	SWISSPROT	HYPOTHETICAL 56.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9085	21602	34532	0.81	2.3E-02	P41988	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9773	22271	35256	0.72	2.3E-02	P50532	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8843	22438	35415	1.4	2.3E-02 AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	
8843	22438	35416	1.4	2.3E-02 AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	
10061	23193	36238	2.37	2.3E-02 F08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	
11628	24070		1.07	2.3E-02 AF158132.1	NT	Mesopneustus enisis fushi tarazu-factor 1 mRNA, complete cds	
11846	24843		5.2	2.3E-02 BE278331.1	EST_HUMAN	601178836F1 NIH MGCG_21 Homo sapiens cDNA clone IMAGE:2648887 5'	
12282	24485	30940	1.69	2.3E-02 BF528482.1	EST_HUMAN	602043628F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'	
12282	24485	30941	1.59	2.3E-02 BF528482.1	EST_HUMAN	602043628F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'	
12392	24552	30907	2.2	2.3E-02 U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds	
12447	25100		3.04	2.3E-02 U11077.1	NT	Dicystostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds	
12680	24940		1.73	2.3E-02	11428388 NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA	
787	13398	25985	3	2.2E-02 AF018267.1	NT	Colombia lira nucleotide diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds	
1783	14373		1.03	2.2E-02	4557448 NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA	
2058	146389	27212	1.33	2.2E-02	282001.1 NT	S. pneumoniae papA gene and open reading frames	
3482	16088		2.1	2.2E-02	AA577785.1 EST_HUMAN	mn248d4.81 NCI_CGAP_Ges1 Homo sapiens cDNA clone IMAGE:1084782 3'	
3708	16399		3.58	2.2E-02	AF083094.1 NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds	
3820	16518	28884	1.11	2.2E-02	AW601317.1 EST_HUMAN	PMID:870340-170100-004-b03 BT1340 Homo sapiens cDNA	
3882	16580	28002	0.85	2.2E-02	274283.1 NT	S.cerevisiae chromosome IV reading frame ORF YDL245c	
5225	17780	30209	0.92	2.2E-02	273597.1 NT	S.cerevisiae chromosome XVI reading frame ORF YPL241C	
7294	18822	32681	3.52	2.2E-02	AV889721.1 EST_HUMAN	AVE889721 GRK8 Homo sapiens cDNA clone GK-BAND03 3'	
8312	20853	33178	2.59	2.2E-02	AL161515.2 NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	
8312	20853	33179	2.56	2.2E-02	AL161515.2 NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	
8744	21283	34205	0.75	2.2E-02	X79468.1 NT	P.wulffia alpha tub 2 mRNA	
8574	22074	35038	0.57	2.2E-02	AJ243025.1 NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5	
9574	22074	35037	0.57	2.2E-02	AJ243025.1 NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5	
8804	22104	35068	1.88	2.2E-02	AB026898.1 NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	
8804	22104	35067	1.88	2.2E-02	AB026898.1 NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	
10108	22801		0.86	2.2E-02	6878140 NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA	
12120	24370		3.85	2.2E-02	AA503553.1 EST_HUMAN	ns47n07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077			4.45	2.1E-02 AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107			5.21	2.1E-02 AF029728.1	NT	Dichotomellum discoidatum histidine kinase C (dhkC) mRNA, complete cds
1306	13090			8.16	2.1E-02 U72073.1	NT	Bacillus subtilis catKLM cluster, CatK (catK), CatL (catL), and spore coat protein CatM (catM) genes, complete cds
1430	14022	26550		1.46	2.1E-02 AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26551		1.46	2.1E-02 AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2842	13428	25834		3.37	2.1E-02 N29286.1	EST_HUMAN	Y44307.1 Soares melanocyte 2N8-HM Homo sapiens cDNA clone IMAGE:284541 6'
3184	14660	27231		0.83	2.1E-02 BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT10546 Homo sapiens cDNA
3184	14660	27232		0.83	2.1E-02 BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT10546 Homo sapiens cDNA clone IMAGE:788121 5'
3843	16246	28721		1.47	2.1E-02 AA461271.1	EST_HUMAN	ZD831058.1 Soares_total_fetus_N251F8_9w Homo sapiens cDNA clone YDL245c
4211	16800	28249		0.77	2.1E-02 Z74263.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4398	18883	28428		0.83	2.1E-02 BF343655.1	EST_HUMAN	8020163008F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4540	17124	28958		1.64	2.1E-02 U44914.1	NT	Bornella burgdorferi plasmid cp32-2, espC and espD genes, complete cds; and unknown genes
4552	17135	28953		1.3	2.1E-02 AI7681127.1	EST_HUMAN	wg81d1.1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371569 3'
4820	17398	28952		5.95	2.1E-02 Y08501.1	NT	A.thaliana mitochondrial genome, part A
4838	17414	28987		0.57	2.1E-02 AA865137.1	EST_HUMAN	eg55912.s1 Gieseler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	28981		0.63	2.1E-02 AI823432.1	EST_HUMAN	wh5465.1x1 NCI CGAP Kit111 Homo sapiens cDNA clone IMAGE:2384528 3'
5321	17883			1.52	2.1E-02 S82470.1	NT	BB1-transfected cell expression-enhanced gene/Human progression-enhanced gene [Human, UMGUC9 bladder carcinoma cell line, mRNA, 1897 nt]
5821	18445	31167		0.8	2.1E-02 AW379526.1	EST_HUMAN	CNA-HT0244-111188-040-h05 HT10244 Homo sapiens cDNA
7128	19468	32284		0.74	2.1E-02 BF088198.1	EST_HUMAN	QV3-GN0058-120500-329-a12 GN0058 Homo sapiens cDNA
8458	20898	33914		0.86	2.1E-02 9780238	NT	Mus musculus sorting neitin 1 (Snt1), mRNA
9422	21931	34979		0.56	2.1E-02 AA984298.1	EST_HUMAN	am83ad7.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
9549	22049	35010		2.41	2.1E-02 AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9549	22049	35011		2.41	2.1E-02 AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35369		1.22	2.1E-02 J28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, release, UmuC MuCB homolog, and UmuD MuCA homolog genes, complete cds; and unknown genes
9893	22468	35452		0.57	2.1E-02 AA884298.1	EST_HUMAN	am83ad7.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
12089	18030			11.53	2.1E-02 Y18213.1	NT	Homo sapiens putative psfHBA pseudogene for hair keratin, exons 2 to 7
12141	24839	30798		1.31	2.1E-02 J34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12552	24855	30871		16.83	2.1E-02 AF183913.1	NT	Axonophyllum brasiliense major outer membrane protein OmaA precursor (omaA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							MER1 repetitive element; IMAGE:3308688 3' similar to contains MER1.13
20	12889	25155	1.34	2.0E-02	BF002832.1	EST_HUMAN	7951c08_x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3308688 3' similar to contains MER1.13
21	12700	25156	9.6	2.0E-02	AW895365.1	EST_HUMAN	QV4-NN0038-270400-187-405 NN0038 Homo sapiens cDNA clone IMAGE:3308688 3' similar to contains MER1.13
280	12837	25422	2.31	2.0E-02	6753635 NT	Mus musculus Dmb homolog 1 (E. cod) (Dmb1), mRNA	as15b10.11 Scores_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:313307.5'
317	12971	25460	2.42	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus Dmb homolog 1 (E. cod) (Dmb1), mRNA
831	13448	25955	1.2	2.0E-02	6753635 NT	Mus musculus Dmb homolog 1 (E. cod) (Dmb1), mRNA	Mus musculus genomic region containing hypervariable minisatellites chromosome 11[1p36.33] of Homo sapiens
1128	13729	28240	1.32	2.0E-02	AL098805.1	NT	Homo sapiens
1241	13839	28358	0.79	2.0E-02	89222391 NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
1241	13839	28357	0.79	2.0E-02	89222391 NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
1914	14499	27053	2.3	2.0E-02	89222453 NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
1914	14499	27054	2.3	2.0E-02	89222453 NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
2824	15378	3.19	2.0E-02	AL161532.2	NT	Mus musculus genome, transcriptome domain (TM), and cytoplasmic domain, (semaphorin) 6B	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3115	12889	25155	1.84	2.0E-02	BF002832.1	EST_HUMAN	7951c08_x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3308688 3' similar to contains MER1.13
3178	15781		1.38	2.0E-02	7905474 NT	Mus musculus genome, transcriptome domain (TM), and cytoplasmic domain, (semaphorin) 6B	MER1 repetitive element; IMAGE:3308688 3' similar to contains MER1.13
3284	15876		1.57	2.0E-02	AF085588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FzF mRNA, complete cds
4073	16874	29135	1.54	2.0E-02	M18095.1	NT	P. vulgaris hydroxypyrolin-rich glycoprotein (HRGP) mRNA, 3' end
5268	17830	30255	1.12	2.0E-02	AF189368.1	NT	Aleutomyces capsulatus cathepsin A (CATA) mRNA, complete cds
6050	18673	31414	0.87	2.0E-02	L35321.2	NT	Dicyostelium discoidium class VII unconventional myosin (myo7) gene, complete cds
7553	20072	32917	1.28	2.0E-02	AP000004.1	NT	Pyracoccus horikoshi OT3 genomic DNA, 777001-894000 nt, position (477)
7553	20072	32948	1.28	2.0E-02	AP000004.1	NT	Pyracoccus horikoshi OT3 genomic DNA, 777001-894000 nt, position (477)
9781	22269		2.5	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10284	22759	35746	1.63	2.0E-02	AI840342.1	EST_HUMAN	war7b02_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315.3'
10522	23060	36070	2.05	2.0E-02	Z735988.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment B37162
11250	23780	36836	2.85	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-hydroxylase, complete cds
11530	23978	37047	1.58	2.0E-02	10947055 NT	Hom sapiens atylin 3, node of Ranvier (Ankyrin G) (ANK3), transcript variant 1, mRNA	Hom sapiens atylin 3, node of Ranvier (Ankyrin G) (ANK3), transcript variant 1, mRNA
11630	23978	37048	1.58	2.0E-02	10947055 NT	Hom sapiens atylin 3, node of Ranvier (Ankyrin G) (ANK3), transcript variant 1, mRNA	as15b10.11 Scores_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:313307.5'
11654	18034	30494	1.91	2.0E-02	AA458538.1	EST_HUMAN	as15b10.11 Scores_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:313307.5'
12138	15376		1.94	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12635	24711		8.4	2.0E-02	T80037.1	EST_HUMAN	yD4c08_x1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24875.5
722	13342	25832	1.93	1.9E-02	AA572784.1	EST_HUMAN	rrf8a07_x1 NCI CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.H1.L1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14251	26785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPTRACLES HOMEOTIC PROTEIN
2083	14884	27234	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2083	14884	27235	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2546	15113	27893	0.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
2830	15546	28021	8.7	1.9E-02	AA713858.1	EST_HUMAN	mm04005.51 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2880	15598	28076	1.56	1.9E-02	AV648689.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLC8LH07 3'
3298	15909		0.75	1.9E-02	AB033611.1	NT	Drosophila melanogaster mitochondrial gene for cytochrome b, complete cds
3671	16272		1.09	1.9E-02	N52250.1	EST_HUMAN	yZ28802.61 Soares_multiple_scenarios_mmRNA clone IMAGE:2243331 3'
3768	16367		6.81	1.9E-02	BE738088.1	EST_HUMAN	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3838594 5'
4121	16714	29170	1.48	1.9E-02	AF141840.1	NT	Mycobacteria initiator VifA1 precursor (VifA1) and VifA2 precursor (VifA2) genes, partial cds
4271	16857	29205	1.57	1.9E-02	P09031	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	29206	1.57	1.9E-02	P09031	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	29875	3.21	1.9E-02	AI452889.1	EST_HUMAN	Y46304.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5157	15113	27893	2.73	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30595	0.83	1.9E-02	AF037432.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5680	18287	30785	1.38	1.9E-02	L47572.1	NT	Meloidogyne gallopannonica peroxinase-2 (PON2) mRNA, complete cds
5939	18581		0.81	1.9E-02	AB0198507.1	NT	Drosophila melanogaster gene for glycerol-3-phosphate dehydrogenase, complete cds
7159	19690	32534	1.41	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7159	19690	32535	1.41	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8506	21045		1.03	1.9E-02	AL162764.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9254	21780	34732	0.94	1.9E-02	BfT316128.1	EST_HUMAN	601698130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9629	22129	35083	0.83	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytocchrome (phyB) gene, complete cds
8858	22453	35435	1.04	1.9E-02	Bf865832.1	EST_HUMAN	601852385F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4078253 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	yy46308.x1 Soares_multiple_scenarios_201HHSF1 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
10151	22846	35839	0.53	1.9E-02	DB4001.1	NT	Synechocystis sp. PCC6803 complete genome; 20/27, 2538000-2844704
11878	24847	30901	4.29	1.9E-02	AF101065.1	NT	Hirudo medicinalis Intermediate filament glairin mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Cα3β fragment
12587	24680	30879	1.7	1.9E-02	X88271.1	NT	H.sapiens MUC18 gene exon 18
368	13017	25500	1.84	1.9E-02	AW771104.1	EST_HUMAN	hn52605.61 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:4139883 5'
714	13335	25821	2.28	1.9E-02	BF308122.1	EST_HUMAN	601694328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1202	13802	28315	1.51	1.9E-02	X17684.1	NT	H.franckei mRNA for myelin basic protein (MBP)
1484	14077	28615	2.3	1.9E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	152611	27828	1.22	1.8E-02 AE004644.1	NT	Pseudomones seruginosa PA01, section 105 of 529 of the complete genome te52a08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2890286 3'	
3247	158559		0.72	1.8E-02 AB056289.1	EST_HUMAN	MR1-OT0011-280390-009-904 OT0011 Homo sapiens cDNA	
3956	165554	28023	1.07	1.8E-02 AW879122.1	EST_HUMAN	MR1-OT0011-280390-009-904 OT0011 Homo sapiens cDNA	
3956	165554	28024	1.07	1.8E-02 AW879122.1	EST_HUMAN	MR1-OT0011-280390-009-904 OT0011 Homo sapiens cDNA	
4160	167532		1.41	1.8E-02 AA861446.1	EST_HUMAN	sk24hd4.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3'	
4521	17105	28651	1.67	1.8E-02 AW83863.1	EST_HUMAN	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA	
5090	178633	30103	1.06	1.8E-02 OG0810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2	
6901	19835	32473	4.27	1.8E-02 P14310	SWISSPROT	HYPOTHETICAL 7.9 kD PROTEIN IN FIXW 5' REGION	
8071	20613	33527	0.81	1.8E-02 U37081.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds	
8404	20944	33988	0.91	1.8E-02 AW903327.1	EST_HUMAN	QV2-NN1073-2220400-159-H09 NN1073 Homo sapiens cDNA	
8449	20889	33907	0.75	1.8E-02 68778943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA	
9413	210222	34870	0.45	1.8E-02 BF241624.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'	
9413	218222	34871	0.45	1.8E-02 BF241624.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'	
9560	220050		2.41	1.8E-02 AA897543.1	EST_HUMAN	sp2209.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1354921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);	
8975	22470	36453	1.72	1.8E-02 BE778274.1	EST_HUMAN	6014683545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868983 5'	
10126	22621	35611	1.12	1.8E-02 X88833.1	NT	Lambgennins mRNA for myomodulin neuropeptide precursor	
11313	230111	36019	1.79	1.8E-02 AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds	
11313	230111	38020	1.79	1.8E-02 AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds	
11480	23830	37001	1.73	1.8E-02 AP00006.1	NT	Pyrococcus horikoshii OT3 genomic DNA_1186001-1485200 nt, position (87)	
11489	23938	37008	3.88	1.8E-02 U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rp2a-3) mRNA, partial cds	
839	13552	28088	0.77	1.7E-02 BE384869.1	EST_HUMAN	601310826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'	
1827	14416	28933	1.89	1.7E-02 AW573183.1	EST_HUMAN	hf34e03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.H1.L1 repetitive element;	
1827	14416	28934	1.89	1.7E-02 AW573183.1	EST_HUMAN	hf34e03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.H1.L1 repetitive element;	
1912	14497		3.27	1.7E-02 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
2159	14738		1.281	1.7E-02 AB004616.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	
2332	14903	27474	4.84	1.7E-02 S74186.1	NT	[microsatellite INRA41] [Ovis aries sheep, Genomic, 361 nt, segment 1 of 2]	
3028	15044	28123	0.84	1.7E-02 AI147615.1	EST_HUMAN	qb22a08.s1 Scores_pregnant_uterus_NiBIPU Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains hm45e04.x1 NCI CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MEF18.b1 MER19 repetitive element;	
3562	16166		4.33	1.7E-02 AW827368.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	
3887	16288		0.65	1.7E-02 PG4929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							ac19104_s1 Stratogene ovary (#637217) Homo sapiens cDNA clone IMAGE:8586927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4248	16836		1.08	1.7E-02 AA888818.1	EST_HUMAN		ye88708_s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:1246417 5'
4278	16834		2.52	1.7E-02 R02500.1	EST_HUMAN		qm08907_x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gba:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4551	17134	29582	0.61	1.7E-02 AI305279.1	EST_HUMAN		h34603_x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
4626	17209	28859	1.44	1.7E-02 AW573183.1	EST_HUMAN		Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4824	17402	28955	1.78	1.7E-02 V00841.1	EST_HUMAN	NT	ox51602_s1 Soares_NHT Homo sapiens cDNA clone IMAGE:1840868 3'
4838	17511		5.59	1.7E-02 AI015078.1	EST_HUMAN		wg5208_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element;
6274	18832	31650	1.8	1.7E-02 AI789242.7.1	EST_HUMAN		oy65103_x1 Soares_fetal_liver_spleen_1NFL_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
6683	18289	32091	1.98	1.7E-02 AI038280.1	EST_HUMAN		Mesaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7112	19452	32268	1.05	1.7E-02 AF180830.1	EST_HUMAN	NT	Home sapiens nebulin (NEB), mRNA
7225	19783	32839	1.98	1.7E-02	8400716_NT		Human apolipoprotein (a) gene, exon 1
7394	19819	32783	1.07	1.7E-02 L07889.1	EST_HUMAN	NT	Human apolipoprotein (a) gene, exon 1
7394	19819	32784	1.07	1.7E-02 L07889.1	EST_HUMAN	NT	Human sapiens hyperin gene, exons 1-50
7724	20232		1.7	1.7E-02 AJ010770.1	EST_HUMAN	NT	Ceenorhabditis elegans cCAF1 protein gene, complete cds
8357	20286	33195	0.97	1.7E-02 U21854.1	EST_HUMAN	DKFZp4340314_1_424 (synonym: hts-2) Homo sapiens cDNA clone DKFZp4340314_5	
9815	22115	35079	1.31	1.7E-02 AL040554.1	EST_HUMAN	CM4-NR1030-04040-130-068 NR1030 Homo sapiens cDNA	
12482	25025	30619	3.35	1.7E-02 AW903482.1	EST_HUMAN	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
537	13168		3.38	1.6E-02 AL021629.1	EST_HUMAN	NT	
1698	14289	26825	1.05	1.6E-02 Y18889.1	EST_HUMAN	NT	Treponema malophilum flaB2, flaB3 and flaD genes for flagellin subunit proteins and CAP protein homologue
2280	14854	27438	2.13	1.6E-02 Q841176	SWISSPROT	UVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	
2280	14854	27439	2.13	1.6E-02 Q841176	SWISSPROT	UVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	
2630	15162	27730	0.98	1.6E-02 AJ008345.1	EST_HUMAN	Homo sapiens KVLQT1 gene	
2689	15227	27789	1.82	1.6E-02 AA484872.1	EST_HUMAN	nes1d06_s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910887	
2718	15275		1.14	1.6E-02 AB014524.1	EST_HUMAN	Homo sapiens mRNA for KIAA0634 protein, partial cds	
3052	15688	28148	0.73	1.6E-02 AF112282.1	EST_HUMAN	Lasaea sp. Isolate 1Bd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product	
3578	16182	28984	5.61	1.6E-02 AW850652.1	EST_HUMAN	IL3-CT0219-1602200-063-C07 CT0219 Homo sapiens cDNA	
3914	16512	28974	0.62	1.6E-02 AL163301.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	16842			1.77	1.E-02 AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NC29, KIF-C1, Fts-binding protein, BING1, tapasin, RacGDS-like, KE22, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Saccharomyces cerevisiae gene, partial?
4298	16974	29424		1.26	1.E-02 AW875407.1	EST_HUMAN	QV24T0012-140100-030-07 PT0012 Homo sapiens cDNA clone IMAGE:22688959 3'
4291	17470	29832		3.99	1.E-02 AT089132.1	EST_HUMAN	WQ346091 X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:22688959 3'
5308	17888			0.61	1.E-02 N80158.1	EST_HUMAN	2A85607.31 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:287444 3'
5907	18432	31153		1.26	1.E-02 6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6752	18345	32152		2	1.E-02 AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7011	18509	32329		1.22	1.E-02 AB0227571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	18509	32330		1.22	1.E-02 AB0227571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7890	20265	33092		0.9	1.E-02 AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8084	20866	33518		0.78	1.E-02 A2777862.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LM domain only 1 protein
8119	20860			1.55	1.E-02 X05151.1	NT	Human apoc-CII gene for preproapolipoprotein C-II
8853	22448			2.92	1.E-02 AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (EPC) mRNA, complete cds
10317	22811	36806		1.17	1.E-02 AA572818.1	EST_HUMAN	mf158p3.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT P22284 TELOKIN. [1];
10317	22811	35800		1.17	1.E-02 AA572818.1	EST_HUMAN	mf19p3.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT P22284 TELOKIN. [1];
10789	24800	36319		2.38	1.E-02 Z94828.1	NT	G. galba microsatellite DNA (LEI0280 (=T16III-E11))
11030	23602	36840		2.5	1.E-02 AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11030	23602	36841		2.5	1.E-02 AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11385	23837	36899		2.38	1.E-02 A373598.1	EST_HUMAN	Q228610 X1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2042442 3'
11855	14884	27438		3.83	1.E-02 Q84178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
11855	14884	27439		3.83	1.E-02 Q84178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
781	13400			51.07	1.E-02 8923734	NT	Homo sapiens transcription factor (HSFA13B084). mRNA
2187	14783	27332		4.36	1.E-02 N39521.1	EST_HUMAN	WZ7607.31 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2219	14784	27337		1.78	1.E-02 AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
3097	15712	28183		0.99	1.E-02 AJ008216.1	NT	Homo sapiens CAACNA1F gene, exons 1 to 48
3097	15712	28184		0.99	1.E-02 AJ008216.1	NT	Homo sapiens CAACNA1F gene, exons 1 to 48
3787	19307	28853		0.98	1.E-02 BF082942.1	EST_HUMAN	MR4-TN115-082802-201-b12 TN0115 Homo sapiens cDNA
4222	16810	29257		0.88	1.E-02 AA160987.1	EST_HUMAN	zr0g10.1 Striatalne HNT neuron (R837233) Homo sapiens cDNA clone IMAGE:8322226 5'
5160	17728			0.78	1.E-02 M13879.1	NT	Human interferulin 2 gene, exons 1 and 2
5405	17303	30374		1.14	1.E-02 AW770341.1	EST_HUMAN	N76H11 X1 NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3007173 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6436	180339	31828	1.31	1.5E-02	Q09771	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7360	188886		1.62	1.5E-02	11467282	NT	Cyanothrix peradicea cyanea, complete genome
7432	186556	328271	1.38	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7816	203598	32265	1.44	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20384	33273	4.16	1.5E-02	11417739	NT	Homo sapiens very-tRNA synthetase 2 (YARS2), mRNA
8764	213033	34224	1.62	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI CGAP Bm87 Homo sapiens cDNA clone IMAGE:4154504 5'
8889	218112		0.51	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
8490	21846	34895	1.64	1.5E-02	D4480.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9725	22223	35188	1.08	1.5E-02	R32867.1	EST_HUMAN	yh54b10r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9725	22223	35200	1.08	1.5E-02	R32867.1	EST_HUMAN	yh54b10r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 6'
10087	23227		1.71	1.5E-02	D28517.1	NT	Rice gene for thioredoxin h, complete cds
11047	23560	36597	2.32	1.5E-02	L40690.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12078	24982		2.26	1.5E-02	AW750834.1	EST_HUMAN	RC4-CR0048-140100-011-c11 CR0048 Homo sapiens cDNA
12838	24712		1.55	1.5E-02	AI763127.1	EST_HUMAN	w06803_x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388493 3 similar to contains Ali repetitive element;contains element MER28 MSR1 repetitive element;
442	13075		1.41	1.4E-02	AE022230.2	NT	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome
1157	13790	26270	4.22	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1298	13853		1.28	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13298		3.36	1.4E-02	U677779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1584	14158		1.09	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAH11 5'
3249	15861	28342	1.81	1.4E-02	AF180969.2	NT	Bifidobacterium longum Na+-H+ antiporter (nhAB), cytosine deaminase, and alpha-galactosidase (egL) genes, complete cds, and N-acetylglucosaminidohydroxylase repressor protein (nagChyRF) gene, partial cds
3445	16053	28530	0.86	1.4E-02	AW014212.1	EST_HUMAN	x0806dd_x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2575783 3
3531	16138	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16138	28817	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16175	28857	0.88	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3717	16318	28786	6.27	1.4E-02	68988918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4587	17170	28814	8.86	1.4E-02	AW862688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4587	17170	28815	8.86	1.4E-02	AW862688.1	EST_HUMAN	EST374781 MAGE resequences, MAGG Homo sapiens cDNA
4787	17348	29797	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4787	17348	29798	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5003	17576	30020	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH MGCG_21 Homo sapiens cDNA clone IMAGE:3842280 5'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17576	30021	6.84	1.4E-02 BE73142.1	EST_HUMAN	601567403FF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'	
6547	19145	31941	4.61	1.4E-02 AA559030.1	EST_HUMAN	nm11c04_s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element	
6547	19145	31942	4.61	1.4E-02 AA559030.1	EST_HUMAN	nm11c04_s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element	
8081	20523		1.97	1.4E-02 AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88162	
8829	21389	34222	1.24	1.4E-02 M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds	
8982	21619	34563	0.89	1.4E-02 AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	
9321	21835	34786	2.48	1.4E-02 BE54561.1	EST_HUMAN	601078238FF1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'	
10451	22945		0.81	1.4E-02 AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018	
11765	24158	36772	12.79	1.4E-02 X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor	
12134	24387		3.62	1.4E-02 AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds	
12433	24574		2.32	1.4E-02 11428988 NT		Homo sapiens sperm associated antigen 7 (SPAG7), mRNA	
1905	14490		1.18	1.3E-02 BE738263.1	EST_HUMAN	601558462FF1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'	
1988	14580	27198	2.55	1.3E-02 AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001	
3250	15862	28343	1.91	1.3E-02 BF697081.1	EST_HUMAN	602129475FF1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'	
3250	15862	28344	1.91	1.3E-02 BF697081.1	EST_HUMAN	602129475FF1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'	
4041	16839		1.68	1.3E-02 AF168288.1	NT	Mus musculus beta-satoylcyan gene, complete cds	
5455	18090	30447	1.48	1.3E-02 AL0498866.2	NT	Mus musculus chromosome X contigB, X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mm04q28orf	
5455	18090	30448	1.48	1.3E-02 AL0498868.2	NT	Mus musculus chromosome X contigB, X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mm04q28orf	
6312	18919	31694	1.4	1.3E-02 U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitor protein (nap1) and survival motor neuron protein (smn) genes, complete cds	
6345	18951	31729	0.88	1.3E-02 M62832.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase active mRNA, complete cds	
7041	18961	30449	1.25	1.3E-02 AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48	
7041	18961	30450	1.25	1.3E-02 AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48	
7578	20694	32871	4.79	1.3E-02 AJ031583.1	EST_HUMAN	ow00g05_x1 Scores_parathyroid_Numor_NbHPA_Homo sapiens cDNA clone IMAGE:1046072 3' similar to contains Alu repetitive element;	
8418	20658	33878	1.63	1.3E-02 AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds	
10108	22603	36583	1.71	1.3E-02 M63707.1	NT	Mouse kidney and liver-regulated protein (KAP) gene, complete cds	
10178	22873	35685	0.77	1.3E-02 AE001504.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome	
10871	23382	36408	4.07	1.3E-02 AW298563.1	EST_HUMAN	xk4e03_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'	
10871	23382	36407	4.07	1.3E-02 AW298563.1	EST_HUMAN	xk4e03_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	25051			2.12	1.3E-02 X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039			2	1.3E-02 Z88117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 25894451 to 2812870
12246	24457			2.77	1.3E-02 86330698	NT	Human Herpesvirus 8B, complete genome
12438	24813			47.13	1.3E-02 AF152238.1	NT	Human sapiens V1b vesprinase receptor (VPR3) gene, complete cds
228	12888			20.25	1.2E-02 X87344.1	NT	Human sapiens DNA, DMB, HLA-Z1, PP2, LMP2, TAP1, LMP7, TAP2, DQB2 and RING3, 8, 13 and 14 genes
977	13025	25511	3.79	1.2E-02 AA056286.1	EST_HUMAN		zf85g011.11 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
478	13111	25601	1.71	1.2E-02 P38886	SWISSPROT		HYPOTHETICAL 17.1 KD PROTEIN IN PUR53 REGION qd688ef12.X1 Scores_bests_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.H L1 repetitive element;
768	13387	26986	8.37	1.2E-02 AI1631522.1	EST_HUMAN		Home sapiens chromosome 21 segment HS21C013
2221	141786	27369	1.85	1.2E-02 AL1631213.2	NT		AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2223	141798	27371	1.15	1.2E-02 AV731704.1	EST_HUMAN		AV731704.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2859432 3'
2487	15052	27824	1	1.2E-02 AW172350.1	EST_HUMAN		X377608.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3454608 5'
2542	15108	27878	1.05	1.2E-02 BE538310.1	EST_HUMAN		601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2542	15108	27879	1.05	1.2E-02 BE538310.1	EST_HUMAN		601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
3135	15749		7.58	1.2E-02 AA075418.1	EST_HUMAN		Zm88603.11 Strategene ovarian cancer (R837219) Homo sapiens cDNA clone IMAGE:5445020 5'
3327	15837	28413	2.02	1.2E-02 R82805.1	EST_HUMAN		y11b08.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:1388903 3'
48338	17513	26959	0.61	1.2E-02 AL161583.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5040	17613	30057	2.65	1.2E-02 US1328.1	NT		Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, RorC gene, and sodium phosphate transporter (NP73) gene, complete cds
5104	17759		1.61	1.2E-02 AB019786.1	NT		Cynops pygmaeus CypUbqT mRNA, partial cds
5224	17808	30230	2.01	1.2E-02 AV731704.1	EST_HUMAN		AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
56227	18549	31275	1.76	1.2E-02 D78589.1	NT	Rana rugosa mRNA for calcitonin, complete cds	
7078	198650	32489	5.21	1.2E-02 AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5	
7334	18861	32725	1.08	1.2E-02 H02197.1	EST_HUMAN	y34h112.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:1506895 3'	
7333	18879	32744	19.46	1.2E-02 AV732093.1	EST_HUMAN		AV732093 HTF Homo sapiens cDNA clone HTFBJCGS 5'
7839	20481	33982	2.3	1.2E-02 Q11205	SWISSPROT		CMP-N-Acetylnueraminate-Beta-Galactosamine-Alpha-2,3-Sialyl Transferase (ALPHA 2,3-ST) (GAL-BETA-1,3-GALACTOSIDE ALPHA-2,3-SIALYL TRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8133	20874	33195	1.2	1.2E-02 AF183612.1	NT	Human sapiens fringe protein mRNA, partial cds	
8133	20874	33598	1.2	1.2E-02 AF183612.1	NT	Human sapiens fringe protein mRNA, partial cds	
8822	21381		1.06	1.2E-02 T76887.1	EST_HUMAN	yst72038.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'	

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9557	22057	35018	2.7	1.2E-02	AB031013.1	NT	Norwalk-like virus gene group 2 gene for capsid protein, complete cds
9558	22088	35053	1.74	1.2E-02	AJ246803.1	NT	Homo sapiens Spasst gene for spastin protein
12446	24582		4.73	1.2E-02	C18118.1	EST_HUMAN	C18118 Human placenta cDNA (T-Fujiiwara) Homo sapiens cDNA clone IMAGE:530924 5'
1312	13906	26426	1.49	1.1E-02	AA070394.1	EST_HUMAN	zm69611.s1 Strategene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3'
1744	14334	26880	1.81	1.1E-02	X75491.1	NT	H.sapiens LPA gene, exon 4
1744	14334	26881	1.91	1.1E-02	X75491.1	NT	H.sapiens LPA gene, exon 4
2082	14863	27233	5.42	1.1E-02	BF345263.1	EST_HUMAN	6020180371 NCI_CGAP_Bm671 Homo sapiens cDNA clone IMAGE:4163908 5'
2902	15519		4.2	1.1E-02	N89523.1	EST_HUMAN	2a40e05.1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:265040 5'
3575	16179	28862	2.88	1.1E-02	AB653508.1	EST_HUMAN	tp95610.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4094	16889		2.1	1.1E-02	BE144687.1	EST_HUMAN	Q92888 DNA-REPAIR PROTEIN COMPLEMENTING XP_F CELL ;
4183	16773		0.61	1.1E-02	AW819788.1	EST_HUMAN	PM3-HT0175-300989-001-h06 HT0175 Homo sapiens cDNA RC3-ST0197-12/2020-015-g11 ST0197 Homo sapiens cDNA
4956	17531	28973	2.09	1.1E-02	AL048383.2	EST_HUMAN	DKFZp588E0824_s1_588 (synonym: hude1) Homo sapiens cDNA clone DKFZp588E0824
6228	18908	31677	1.03	1.1E-02	U684480.1	NT	Bacillus subtilis SpoV(K) (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC (ynaC), YneD (yneD), YneF (yneF), YneG (yneG), YneH (yneH), YneI (yneI), YneJ (yneJ), YneL (yneL), YneM (yneM), YneN (yneN), YneO (yneO)
7594	20108	322883	2.55	1.1E-02	BE14861.1	EST_HUMAN	RC1-HT0256-10330-016-h07 HT0256 Homo sapiens cDNA
8189	20740	33882	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONINE (MT-1/MT-2)
8189	20740	33853	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONINE (MT-1/MT-2)
8574	21113	34032	0.64	1.1E-02	AW886160.1	EST_HUMAN	QV3-BN045-226308-128-h02 BN045 Homo sapiens cDNA
8756	21296	34216	0.69	1.1E-02	C94803.1	EST_HUMAN	C04803 Human heart cDNA (Yoshizumura) Homo sapiens cDNA clone 3NHC4040
8833	21372	34297	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9842	22340	35322	2.07	1.1E-02	AA082578.1	EST_HUMAN	2024601.1 Strategene neuroepithelium NT2RAMI 897234 Homo sapiens cDNA clone IMAGE:548328 5'
10006	22501	35492	3.79	1.1E-02	AA314665.1	EST_HUMAN	EST188494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10853	23379	36398	3.88	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24116		2.67	1.1E-02	AA688239.1	EST_HUMAN	ab7711.1 Strategene fetal retina 897202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element
12512	16773		1.87	1.1E-02	AW81788.1	EST_HUMAN	RC3-ST0197-12/2020-015-g11 ST0197 Homo sapiens cDNA
7	12886	25144	6.97	1.0E-02	AW846120.1	EST_HUMAN	MR3-CTD178-111086-003-g10 CT0178 Homo sapiens cDNA
1570	14163	26884	2.33	1.0E-02	AW386128.1	EST_HUMAN	CM2-HT0177-041086-017-h112 HT0177 Homo sapiens cDNA
2806	15168		1.9	1.0E-02	AA808389.1	EST_HUMAN	oc22H08_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350485 3'
3126	15740	28239	3.7	1.0E-02	BER855556.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3302	15913	28391	1.41	1.0E-02	BE988898.1	EST_HUMAN	80164987TR1 NIH_MIGC_74 Homo sapiens cDNA clone IMAGE:3983688 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	16162			0.63	1.0E-02 AW845621.1	EST_HUMAN	MRO-CT0080-0810582-003-h10 CT0080 Homo sapiens cDNA
3950	165448	28016	0.68	1.0E-02 AF085086.1	EST_HUMAN	IAB921 Human fetal liver cDNA library Homo sapiens cDNA	
4891	17468	29921	5.12	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Crtfr2), mRNA
4970	17544	28986	6.03	1.0E-02 IR08567.1	EST_HUMAN	YR54H01_1f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:188833 5'	
5221	17783	30204	1.01	1.0E-02 AF216910.1	NT	Homo sapiens atrachin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced	
5317	17879	30288	0.98	1.0E-02 P06599	SWISSPROT	EXTENSIN PRECURSOR	
5394	17952		16.85	1.0E-02 AV723678.1	EST_HUMAN	AV723678 HTB Homo sapiens cDNA clone HT1BAPPF08 5'	
5445	18000		3.87	1.0E-02 D346321	NT	Arabidopsis thaliana acc2 gene for acetyl-CoA carboxylase, partial cds	
5610	18239	30883	0.8	1.0E-02 H526891.1	EST_HUMAN	YU38H11_1f1 Soares ovary tumor NbHOT1 Homo sapiens cDNA clone IMAGE:2356941 5'	
5921	18543	31269	0.7	1.0E-02 AF308388.1	NT	Mus musculus transcription complex subunit NF-ATC4 (Nfatc4) gene, exons 1 and 2	
6284	18872	31642	0.89	1.0E-02 AF257303.1	NT	Mus musculus synaptobrevin II (Sy2) gene, complete cds	
6328	19834	31709	2.67	1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA	
6328	18834	31710	2.67	1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA	
6859	18693	32425	2.22	1.0E-02 Z28842.1	NT	Z.mays U35rRNA pseudogene	
8240	20781		0.46	1.0E-02 Z28107.1	EST_HUMAN	S.cerevisiae chromosome XI reading frame ORF YKL107W	
9314	21828	34778	4.29	1.0E-02 BF038331.1	EST_HUMAN	601458570F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3863177 5'	
9314	21828	34779	4.29	1.0E-02 BF038331.1	EST_HUMAN	Critchidia fasciata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product	
11143	23651		2.17	1.0E-02 AF157559.1	NT		
11246	23778	38833	2.02	1.0E-02 AV78016.1	EST_HUMAN	AV780016 MDS Homo sapiens cDNA clone MDSBDC10 5'	
11785	25110		2.16	1.0E-02 Q62203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A62)	
11847	24862	30705	4.64	1.0E-02 AW835521.1	EST_HUMAN	RC2-DT0007-1/20200-016-h02 DT0007 Homo sapiens cDNA	
11861	24822		6.07	1.0E-02 S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds	
12224	24898		1.53	1.0E-02 AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7	
12422	24882		4.42	1.0E-02 X62654.1	NT	H.sapiens gene for Me491/C363 antigen MER22 MER22 repetitive element;	
826	13539	28057	3.16	9.0E-03 A1786126.1	EST_HUMAN	WH2098X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element	
1307	13901		1.26	9.0E-03 BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'	
2439	15008	27578	3.82	9.0E-03 AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 59	
2449	15016	27598	0.87	9.0E-03 AF08634.1	NT	Mus musculus MH-C class III protein RP1 (Rp1) mRNA, partial cds	
2831	15547	28022	0.61	9.0E-03 AI251744.1	EST_HUMAN	QH80F98X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'	
2831	15547	28023	0.61	9.0E-03 AI251744.1	EST_HUMAN	QH80F98X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'	
3731	16332	28788	0.8	9.0E-03 J05184.1	NT	S.acidocalcarinus thermophilus gene, complete cds	
5978	18598		1.17	9.0E-03 AI809782.1	EST_HUMAN	WT7704X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381683 3'	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6741	19335		4.24	9.0E-03	BE745888.1	EST_HUMAN	NIH_MGC_9 Homo sapiens cDNA clone IMAGE:36334762 5'
7487	20010	32876	0.73	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7816	20359		0.83	9.0E-03	AL038801.1	EST_HUMAN	DKFZp424L0412_11_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp424L0412_5'
8191	20732		0.58	9.0E-03	AF222381.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial exons, alternatively spliced
9759	22257	35240	0.6	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
9776	22274	35259	1.28	9.0E-03	P20808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10985	23386		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
109891	23412	38431	1.71	9.0E-03	BE395380.1	EST_HUMAN	NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36321811 5'
11505	23984	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens proopiomelanin (GAL1) gene, exons 1, 2, and 3
11505	23984	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens proopiomelanin (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-009 HT0452 Homo sapiens cDNA
12221	25105		38.8	9.0E-03	BE348385.1	EST_HUMAN	hw17009_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31831811 3'
12319	24509	30943	1.38	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21Q087
12539	24849		31.67	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-009 HT0452 Homo sapiens cDNA
527	131189		2.87	8.0E-03	AA723007.1	EST_HUMAN	zr30e03_s1 Scores_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element
1028	13837	28152	35.57	8.0E-03	AF106886.1	NT	Homo sapiens acetylglucosaminidase gene, complete cds
22203	14779	27351	1.28	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21Q083
3351	15859	28438	0.89	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3404	16013	28492	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3738	16339	28805	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3738	16339	28806	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16890	28971	1.19	8.0E-03	BE84049.1	EST_HUMAN	QVO-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4472	17053	28955	6.38	8.0E-03	BP7383327.1	EST_HUMAN	CM4-NN0119-300800-223-b05 NN0119 Homo sapiens cDNA
5378	17837	30050	1.02	8.0E-03	U02870.1	NT	Proteobacteria_wickerhamii 283-11 complete mitochondrial DNA
5410	17857	30316	0.88	8.0E-03	P01871	SWISSPROT	IG MU CHAIN C REGION
5714	18340	30848	2.89	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KEE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial?
6348	24762	31170	1.34	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (2/7)
6846	18436	32251	4.45	8.0E-03	P56577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6899	19497		1.72	8.0E-03	V0110.1	NT	Human ERK1/2 (strain MM) genome. (Closely related to SV40.)
7259	19787	32633	1.8	8.0E-03	M17187.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20067			1.84	8.0E-03 AB038267.1	NT	Turkops truncatus mRNA for p40-phox, complete cds
8816	21355	34279		0.62	8.0E-03 P88160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (ISP-G) (PERLECAN) (PLC)
8841	21380	34304		3.73	8.0E-03 AW880892.1	EST_HUMAN	MR1-ST0111-111188011-h08 ST0111 Homo sapiens cDNA
8910	21448	34370		0.68	8.0E-03 9789936	NT	Mus musculus fusion 2 (Human) (Fus2), mRNA
8859	22358			4.76	8.0E-03 BE085509.1	EST_HUMAN	QVI-8T0677-040400-131-003 B110677 Homo sapiens cDNA
10884	23385			3.01	8.0E-03 Z48052.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11259	23789	36945		1.97	8.0E-03 AAB28817.1	EST_HUMAN	od8ba08_s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11259	23789	36846		1.97	8.0E-03 AA828817.1	EST_HUMAN	od8ba08_s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11562	24009	37079		4.90	8.0E-03 AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11713	24123			2.81	8.0E-03 M68035.1	NT	Oryctolagus cuniculus eIF-2α kinase mRNA, complete cds
11761	24154			5.88	8.0E-03 AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25833		14.03	7.0E-03 AF087183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
723	13343	25834		14.03	7.0E-03 AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13822	26137		5.78	7.0E-03 AF243378.1	NT	Glycine max glutathione S-transferase GST_21 mRNA, partial cds
1155	13758	26268		3.21	7.0E-03 AV73712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZE10 6'
1408	14001			1.28	7.0E-03 Q81000	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1439	14032	28560		4.09	7.0E-03 AA688288.1	EST_HUMAN	ab78608_s1 Stratego fetal retina 837202 Homo sapiens cDNA clone IMAGE:853145 3'
1550	14142	28676		3.14	7.0E-03 AW303569.1	EST_HUMAN	xx21002_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2613739 3'
2287	15482	27447		2.12	7.0E-03 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3614	16217	28686		0.58	7.0E-03 AI150273.1	EST_HUMAN	qf34h02_x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3830	16430	28892		0.91	7.0E-03 AW444463.1	EST_HUMAN	UH-B13-ab2-c-10-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733891 3'
3985	16483	29845		1.01	7.0E-03 AF188344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4091	16430	28892		0.63	7.0E-03 AW444463.1	EST_HUMAN	UH-B13-ab2-c-10-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733891 3'
4704	17296			1.1	7.0E-03 AW630888.1	EST_HUMAN	hh898d5_y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2888886 5'
5125	17687			2.08	7.0E-03 AL168278.2	NT	Homo sapiens chromosome 21 segment HS21C078
							yr82q01_r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
5695	18905			0.70	7.0E-03 H71108.1	EST_HUMAN	gb:X14723 CLUSTERIN PRECURSOR (HUMAN)
6260	24790			5.32	7.0E-03 AW881058.1	EST_HUMAN	RC1-CT0286-050400-018-008 CT0286 Homo sapiens cDNA
8456	19057	31842		1.45	7.0E-03 W88251.1	EST_HUMAN	zz33f10_r1 Scores_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:3424755
6658	19254	32056		2.88	7.0E-03 AA3227128.1	EST_HUMAN	EST30874 Col1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
66881 19277	32080	0.82	7.0E-03 BE857585.1	EST HUMAN	7634b10_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q133887		
7139 18519	32341	2.12	7.0E-03 BE828133.1	EST HUMAN	Q13387 HYPOTHETICAL PROTEIN_384D8_2; contains TAR1.12 TAR1 repetitive element ; CM2-CT0478-230803-347-b11 C10478 Homo sapiens cDNA		
75229 20049	32921	5.78	7.0E-03 Z35839.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w		
75229 20049	32922	5.78	7.0E-03 Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w		
7789 20332	33238	0.54	7.0E-03 AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBP1 on chromosome 21q22, segment 3/3		
7789 20332	33239	0.64	7.0E-03 AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBP1 on chromosome 21q22, segment 3/3		
8055 20597	33504	2.38	7.0E-03 BE175987.1	EST HUMAN	RCS-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA		
8318 21832		0.6	7.0E-03 AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes		
8513 22013	34972	0.87	7.0E-03 N52378.1	EST HUMAN	IMAGE:2480686 3' similar to contains yM8C10_x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:2480686 3' similar to contains		
86336 22136	35101	2.48	7.0E-03 P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)		
86336 22136	35102	2.48	7.0E-03 P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)		
10207 22702		0.99	7.0E-03 AV687378.1	EST HUMAN	AV687379 GKC Homo sapiens cDNA clone GKCAF07 5'		
10381 22875		0.83	7.0E-03 AJ798734.1	EST HUMAN	wc3768_x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'		
10706 23235	34248	3.46	7.0E-03 AR008852.1	NT	Bos taurus mRNA for NDP52, complete cds		
10780 23304	36311	1.61	7.0E-03 AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-20		
10780 23304	36312	1.61	7.0E-03 AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29		
10830 23448		1.66	7.0E-03 AJ242804.1	NT	Sporobolus stapfianus mRNA for putative glycine and proline-rich protein		
12273 25065					yf15h01_x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:242833 3' similar to contains		
12273 25065					Alu repetitive element		
122281 24484		1.58	7.0E-03 BE283253.1	EST HUMAN	60114515184F2 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3160476 5'		
12382 24549		1.86	7.0E-03 Y17455.1	NT	Homo sapiens LSPR2 gene, penultimate exon		
12527 25092		1.38	7.0E-03 AL163390.2	NT	Homo sapiens chromosome 21 segment HS21C100		
126884 24734		3.16	7.0E-03 AW888110.1	EST HUMAN	RCD-SN0052-110400-021-604 SN0052 Homo sapiens cDNA		
1283 13879	28400	10.8	8.0E-03 AW511148.1	EST HUMAN	hd22205_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN_O76469 ORPHAN NUCLEAR RECEPTOR PXR ;		
1283 13879	28401	10.8	8.0E-03 AW511148.1	EST HUMAN	hd22205_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN_O75469 ORPHAN NUCLEAR RECEPTOR PXR ;		
2890 16352	27821	1.82	8.0E-03 AF112374.1	NT	Danio rerio odontor receptor gene cluster		
2916 15533	28004	3.54	8.0E-03 AA758135.1	EST HUMAN	ah76611_x1 Soares_NHT_Homo sapiens cDNA clone 1321772 3'		
2916 15533	28005	3.54	8.0E-03 AA758135.1	EST HUMAN	ah76611_x1 Soares_NHT_Homo sapiens cDNA clone 1321772 3'		
3283 15894		2.17	8.0E-03 HT75890.1	EST HUMAN	yt77n04_x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:211351 5'		

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3344 15864			0.79	6.0E-03 AF190338.1	NT	Notocus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product	
3420 16037	28518		1.14	6.0E-03 U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septapeptidin reductase and vasotocin genes, complete cds	
3429 16037	28519		1.14	6.0E-03 U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septapeptidin reductase and vasotocin genes, complete cds	
3800 16204			1.13	6.0E-03 W37985.1	EST_HUMAN	2x13a011_x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:3221725'	
3721 16322	28789		2.6	6.0E-03 BF510988.1	EST_HUMAN	UH-B14-apm-o-08-0-U1s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30807754 3'	
3757 16358	28828		1.53	6.0E-03 BE077358.1	EST_HUMAN	RC1-BT10508-2604008-014-a07 BT10508 Homo sapiens cDNA	
3845 16444	28905		1.14	6.0E-03 6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp1), mRNA	
3895 16893	28068		0.83	6.0E-03 AW847284.1	EST_HUMAN	RC0-C70204-240598-021-b10 C710204 Homo sapiens cDNA	
4030 16828			0.82	6.0E-03 BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:28385113 5'	
4419 17004			1.1	6.0E-03 NS8840.1	EST_HUMAN	y62210_x1 Soares_multiple_scleratosis_ZnBt-HASp Homo sapiens cDNA clone IMAGE:2781783'	
4454 17040			1.58	6.0E-03 A1016883.1	EST_HUMAN	o633c11_x1 Soares_testis_NHT Homo sapiens cDNA 5' end similar to EST containing Alu repeat	
4805 17383	28833		8.21	6.0E-03 AA32242.1	EST_HUMAN	EST27118_Cerebellum_II_Homo_sapiens cDNA clone IMAGE:1639124;3'	
5280 17852			0.82	6.0E-03 L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22	
6301 24761	31680		0.72	6.0E-03 8527521	NT	Vanda virus, complete genome	
6805 18840	32478		0.73	6.0E-03 O14884		SWISSPROT SYNAPSIN III	
6839 18047	30469		0.72	6.0E-03 BE253748.1	EST_HUMAN	60111235F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33393172 5'	
7842 20154	33040		0.76	6.0E-03 AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds	
7774 20263	33180	24.22	6.0E-03 AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55		
7799 20342	33251		6.91	6.0E-03 AJ033980.1	EST_HUMAN	cw13a04_x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:16466870 3' similar to contains MER10_b1 MER10 repetitive element;	
7915 20457	33383	2.45	6.0E-03 AW790837.1	EST_HUMAN	RC0-UM00857-21-03000-032-g02 UN/0051 Homo sapiens cDNA		
7880 20532			1.59	6.0E-03 BF0388188.1	EST_HUMAN	601454615F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3838626 5'	
9473 21872	34821		8.46	6.0E-03 D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) Virus mRNA for fusion protein	
8958 22451			2.15	6.0E-03 AJ432981.1	EST_HUMAN	622cd2-x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	
10067 22582	35557		0.73	6.0E-03 AJ011184.1	NT	Bacillus subtilis ferD gene	
10197 22892			0.91	6.0E-03 AF084555.1	NT	Homo sapiens chalcocyst acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds	
10303 22787	35788		0.63	6.0E-03 X68386.1	NT	M. thermophila/citricum complete plasmid pF1 DNA	
10623 23155	36168		2.04	6.0E-03 AW982164.1	EST_HUMAN	EST374237 MAGE sequences, MAGG Homo sapiens cDNA	
10690 23220			2.23	6.0E-03 11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1_0728	23252	36269	2.16	8.0E-03	AI420788.1	EST_HUMAN	ts81c12_x1 NCI_CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE :
10981	23252	36270	2.16	8.0E-03	AI420788.1	EST_HUMAN	ts81c12_x1 NCI_CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE :
10982	23382	36401	2.08	8.0E-03	U14553.1	NT	<i>Mus musculus</i> zinc-finger protein mRNA, complete cds
11630	24072	37134	1.57	8.0E-03	H70288.1	EST_HUMAN	y85f01_r1 Soares total liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:SF-GD PIG P14332 6'-PHOSPHOGLUCONATE DECARBOXYLATING :
11632	24195		3.52	8.0E-03	AF010486.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11636	24848		5.1	8.0E-03	AE000853.1	NT	<i>Methanobacterium thermophilum</i> from bases 4281982 to 4502896 (section 39 of 148) of the complete genome
12039	24914		3.02	8.0E-03	UJ0790.1	NT	Pneumocystis carinii 1 sp. ratif guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
12088	24357		1.61	8.0E-03	Q62208	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24581		1.49	8.0E-03	BE788018.1	EST_HUMAN	601462621F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:38853988 5'
12418	24571		1.52	8.0E-03	AJ245480.1	NT	<i>Brassica napus</i> sgg gene for S-locus glycoprotein, cutiver T2
12556	24942		1.6	8.0E-03	X74807.1	NT	R.norvegicus VEGP2 gene
229	12889	23375	5.16	5.0E-03	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING3, 9, 13 and 14 genes
697	13320	25806	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; amineacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
697	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; amineacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
698	13320	25808	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; amineacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1151	13754	25284	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH43
2706	15263	27830	2.77	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2862	15573	28057	0.68	5.0E-03	BE386057.1	EST_HUMAN	601194786F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35398788 5'
3170	15794	28256	4.54	5.0E-03	187623.1	EST_HUMAN	yc81f08.51 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22385 3'
3189	15801		2.22	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	R17184.1	EST_HUMAN	y86g02.51 Soares breast 2NBHbst1 Homo sapiens cDNA clone IMAGE:155868 3'
3318	15823		0.98	5.0E-03	AJ287387.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3728	18328	28785	5.04	5.0E-03 AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085	
3762	18363	28831	4.89	5.0E-03 AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (panB) gene, complete cds	
3822	18422	28884	0.68	5.0E-03 U38914.1	NT	Citrus sinensis seed storage protein cithin mRNA, complete cds	
4043	18841		1.78	5.0E-03 AA288875.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end	
4204	18793	29239	0.57	5.0E-03 AJ002125.1	NT	Matrix domestica Ztx type gene	
4392	18678	29425	0.88	5.0E-03 H78355.1	EST_HUMAN	YU78310.1 Soay sheep fetal liver spleen 1NFES Homo sapiens cDNA clone IMAGE:2400683 5'	
4394	18422	28884	0.71	5.0E-03 U38914.1	NT	Citrus sinensis seed storage protein cithin mRNA, complete cds	
4670	17552	29704	0.68	5.0E-03 U46891.1	NT	Human putative chromatin structure regulator (SUP16H) mRNA, complete cds	
4714	17285	28739	0.8	5.0E-03 AJ131016.1	NT	Homo sapiens SCL gene locus	
4828	17408	28860	1.72	5.0E-03 AI752387.1	EST_HUMAN	cn15c02x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBc_cn15c02 random	
5067	17840	30083	1.02	5.0E-03 P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)	
5391	17849	30362	0.95	5.0E-03 AF176688.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds	
5964	18886	31320	7.68	5.0E-03 P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)	
						PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)	
6195	18805	31574	2.33	5.0E-03 C00507	SWISSPROT	Chlamydomonas AR39, section 62 of 64 of the complete genome	
6220	18838		0.91	5.0E-03 AE002234.2	NT		
6708	18602		10.88	5.0E-03 RE200091.1	EST_HUMAN	600944384T1 NIH 3T3	
6832	18040	30483	6.39	5.0E-03 AB025024.1	NT	Mus musculus AMD 1 gene for S-adenosylmethionine decarboxylase, complete cds	
7108	19446		0.85	5.0E-03 AB033267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds	
7595	20108		1.16	5.0E-03 AW854327.1	EST_HUMAN	RC3-CT0255-031089-01-07 CT0255 Human sepius cDNA	
7744	20252	33149	7.43	5.0E-03 AB016916.1	NT	Homo sapiens MASL1 mRNA, complete cds	
8182	20703	33618	1	5.0E-03 AW855807.1	EST_HUMAN	RC8-CT0281-081108-01-06 CT0281 Human sepius cDNA	
8182	20703	33619	1	5.0E-03 AW855807.1	EST_HUMAN	RC8-CT0281-081108-01-06 CT0281 Human sepius cDNA	
8181	20722	33638	2.28	5.0E-03 P48932	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	
8548	21087		6.38	5.0E-03 M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end	
8742	21261	34204	1.47	5.0E-03 D807723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)	
8870	21408	34333	0.68	5.0E-03 MP25080.1	NT	Rabbit interoglobin (IGL) gene, exon 1	
9503	22003	34980	0.45	5.0E-03 P33750	SWISSPROT	SOF1 PROTEIN	
9753	22251	35234	0.82	5.0E-03 L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds	
9881	22378	35354	0.77	5.0E-03 AW821888.1	EST_HUMAN	RC0-ST0378-210100-0322-002 ST0378 Homo sapiens cDNA	
10082	22557	35552	0.49	5.0E-03 AA533143.1	EST_HUMAN	Y446n10.1 NCI CGAP_P19 Homo sapiens cDNA clone IMAGE:585587	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10238	22731	35722	0.92	5.0E-03	76822557	NT	Homo sapiens PRO0471 protein (PR00471), mRNA
10599	23133		10.33	6.0E-03	T10598.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10831	23163	36175	2.28	5.0E-03	D28273.1	NT	Unknown nitrogen-fixing bacteria rifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23240	36354	2.94	5.0E-03	AW170334.1	EST_HUMAN	xn59-05_x1 Scores_NHCeC_center_tumor Homo sapiens cDNA clone IMAGE:26898040 3' similar to contains L1_12L1 repetitive element;
10820	23439	36450	2.02	6.0E-03	T491B3.1	EST_HUMAN	yb00504.1 Strategene placenta (#8377225) Homo sapiens cDNA clone IMAGE:706886 5'
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	bz46c04.1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
11972	25054		8.12	5.0E-03	AF047874.1	NT	Gallus gallus glycerophosphate dehydrogenase mRNA, complete cds
12111	24372		21.73	5.0E-03	AF067263.1	NT	Brugia malayi Y chromosome marker
12217	24440		1.81	5.0E-03	L0347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-64, complete cds
12250	24481		1.78	5.0E-03	AA456507.1	EST_HUMAN	zx75a03_s1 Scores ovary tumor Nb/HOT Homo sapiens cDNA clone IMAGE:808548 3' similar to SW-DXL2_MOUSE_P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT :
12283	24558		5.48	5.0E-03	BF572322.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12473	24598	30883	2.21	5.0E-03	AW448109.1	EST_HUMAN	UH-B12-ah4-08-0-U1_s1 NCI CGAP_S25 Homo sapiens cDNA clone IMAGE:2734215 3'
12498	24832		1.42	5.0E-03	Q02398	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (L LONG-CHAIN COLLAGEN)
253	12613	25397	2.58	4.0E-03	AW500198.1	EST_HUMAN	U-HFB-N0-eh0-h-04-0-U1_s1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
343	12885	25460	1.77	4.0E-03	R48482.1	EST_HUMAN	Y051604_s1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:359888 3'
468	13101	25594	0.89	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE (PI3-KINASE) (PTK3)
629	13258	25730	3.12	4.0E-03	AA030339.1	EST_HUMAN	mt75g12_s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582586 3'
910	13523	26043	1.75	4.0E-03	R48482.1	EST_HUMAN	Y051604_s1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:359888 3'
944	13557		3.19	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1190	13791	26302	25.91	4.0E-03	AA08977.1	EST_HUMAN	Z081608_s1 Strategene clone (#8377204) Homo sapiens cDNA clone IMAGE:310888 5'
1211	13811	26325	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1346	13841	26463	1.4	4.0E-03	AA284374.1	EST_HUMAN	ZS58801_s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:701736 5'
1630	14222		1.08	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB08 5'
1779	14269	26913	2.74	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
2082	14642	27217	14.12	4.0E-03	AA08977.1	EST_HUMAN	281608_s1 Strategene clone (#8377204) Homo sapiens cDNA clone IMAGE:510888 5'
2289	14983		1.62	4.0E-03	BE410558.1	EST_HUMAN	60130416F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2317	14889	27484	2.63	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), actin-depolymerizing protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), actin-depolymerizing protein >
2715	15272	27838	3.14	4.0E-03	AJ277385.1	NT	Homo sapiens polyamines-containing C14orf4 gene
2715	15272	27839	3.14	4.0E-03	AJ277385.1	NT	Homo sapiens polyamines-containing C14orf4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3282	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151284-003-H08 HT0340 Homo sapiens cDNA
3282	15874	28358	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151284-003-H08 HT0340 Homo sapiens cDNA
3583	16197	28889	0.85	4.0E-03	AW188428.1	EST_HUMAN	xp8804.1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:26685270 3'
3583	16197	28890	0.85	4.0E-03	AW188428.1	EST_HUMAN	xp8804.1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:26685270 3'
36885	16228	28735	0.63	4.0E-03	Q13608	SWISSPROT	OLFACTOORY RECEPTOR 5H (OLFACTOORY RECEPTOR-LIKE PROTEIN OLF1)
36886	16237	28787	0.63	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCALDO2 3'
4067	16683	28350	1.83	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4323	16909	28350	1.88	4.0E-03	AJ786727.1	EST_HUMAN	W18760.1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400274 3'
5307	17699	30281	2.1	4.0E-03	AW103719.1	EST_HUMAN	xp88303.1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1_H1 L1
5354	17614	30329	1.17	4.0E-03	AA688895.1	EST_HUMAN	Z168801.1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4360009 3'
5433	17689	30395	1.19	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5480	18114	30523	1.36	4.0E-03	AF003859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5598	18226	30873	21.16	4.0E-03	AF168625.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
6683	18585	31319	3.31	4.0E-03	P04196	SWISSPROT	(HPRG)
5985	18697	31321	1.58	4.0E-03	P21848	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
6042	18691	31400	0.87	4.0E-03	AL133871.1	EST_HUMAN	DKFZp76111014_11761 (synonym: hmyr2) Homo sapiens cDNA clone DKFZp76111014 5'
6235	18944		3.41	4.0E-03	U22180.1	NT	Rattus norvegicus opsh gene, complete cds
6381	18985	31765	0.88	4.0E-03	AW560572.1	EST_HUMAN	hg46c07.1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2248852 3'
6451	18942	31837	1.85	4.0E-03	BE548453.1	EST_HUMAN	601078016F1 NIH_MSC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6775	19367	32179	1.04	4.0E-03	AA813722.1	EST_HUMAN	432211.1 Scares_tests_NHT Homo sapiens cDNA clone 1392045 3'
6872	18606	32440	1.51	4.0E-03	U78468.1	NT	Lycoperdon esculentum Knotted 3 protein (TKN2) mRNA, complete cds
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7130	19470	32289	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7249	19778	32633	5.45	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7459	18852	32847	1.14	4.0E-03	AI681483.1	EST_HUMAN	b37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:22718143'
7461	18894	32849	0.95	4.0E-03	BE970170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:32840493 3'
7883	20425	33334	0.63	4.0E-03	Q9T1B2	SWISSPROT	ADAM-TS 6 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
7882	20534	33438	4.22	4.0E-03	AF111044.1	NT	Dicytostatinum A1A development protein DG1122 (DG1122) genes, partial cds
8145	20689	33588	1.94	4.0E-03	78820987	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8848	21187	34105	6.89	4.0E-03	AI553983.1	EST_HUMAN	hsab11.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8821	21360		4.48	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8830	21369	34283	3.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9840	22338	35310	0.78	4.0E-03	HS0864.1	EST_HUMAN	yp42g12.r1 Scares retina N2b5-HR Homo sapiens cDNA clone IMAGE:180150 5'
10278	22773	35782	0.7	4.0E-03	AL161658.2	NT	Archidopsis thienae DNA chromosome 4, contig fragment No. 55
11009	23523	36557	6.03	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11383	23845	36909	1.69	4.0E-03	AI208703.1	EST_HUMAN	q958c05.x1 Scares testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11383	23845	36910	1.69	4.0E-03	AI208703.1	EST_HUMAN	q958c05.x1 Scares testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11607	24050	37119	1.62	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
11838	25071		10.45	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180809-002-b08 BN0138 Homo sapiens cDNA
11882	24284		1.62	4.0E-03	BE288280.1	EST_HUMAN	801118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:30280893 5'
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	U1-HF-BN0-dp-g-04-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080822 5'
12294	24493		3.86	4.0E-03	BF224125.1	EST_HUMAN	7q74c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3
12341	24875		2.24	4.0E-03	AW614588.1	EST_HUMAN	elementcontains element MER31 repetitive element;
12352	24532		3.01	4.0E-03	AW819141.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:28539332 3' similar to contains element LTR5 repetitive element;
384	13040	25531	1.73	3.0E-03	AF01920.1	NT	RC3-ST0281-240400-015-03 ST0281 Homo sapiens cDNA
912	13525	26044	5.57	3.0E-03	AF01920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
							Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1701	14294	26829	2.85	3.0E-03	AA468110.1	EST_HUMAN	nc73cd5.x1 NCI_CGAP_Pt2 Homo sapiens cDNA clone IMAGE:782884 similar to contains Alu repetitive element;
2288	14871		1.76	3.0E-03	AF055068.1	NT	Homo sapiens MHC class 1 region
2333	14804		4.14	3.0E-03	732521.1	NT	S.cerev (cv. Hale) mRNA for inositolphosphate isomerase
2334	14805	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2334	14805	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2448	15015	27587	1.13	3.0E-03	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3022	15538		0.68	3.0E-03	Y08008.1	NT	Arabidopsis thaliana np017 gene
3119	15733	28203	3.25	3.0E-03	BE370298.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606833 5'
3185	15798	28270	3.21	3.0E-03	AW802287.1	EST_HUMAN	IL2-LUM0078-240300-058-D03 U00078 Homo sapiens cDNA
3464	18074	28544	2.13	3.0E-03	U34806.1	NT	Mus musculus alpha-1(XVII) collagen (COL1A1) gene, exon 1 and 2
3473	18070		7.31	3.0E-03	Y12500.1	NT	C.elegans semdc gene
4049	18946	28114	7.57	3.0E-03	AV762382.1	EST_HUMAN	AV762382 MDS Homo sapiens cDNA clone MDSESBG01 5'
4049	18946	29115	7.57	3.0E-03	AV762382.1	EST_HUMAN	AV762382 MDS Homo sapiens cDNA clone MDSESBG01 6'
4109	16703	28158	1.75	3.0E-03	A1792278.1	EST_HUMAN	an04f09.6 Cesslier Wilms tumor Homo sapiens cDNA clone IMAGE:1156889 5'
4485	17070	28520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdf1 gene
4580	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	Hs68p08x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4816	17189	28647	5.73	3.0E-03	AI632614.1	EST_HUMAN	x08_P10J13 cancrum Homo sapiens cDNA 3'
4980	17535	28677	2.45	3.0E-03	A1732754.1	EST_HUMAN	ab18a08x5 Strategene lung (#807210) Homo sapiens cDNA clone IMAGE:8411423' similar to contains Abu repetitive element;
4979	17553	28695	6.1	3.0E-03	BE787945.1	EST_HUMAN	601482175F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885483 5'
5068	17842	30084	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus cuniculus sod gene
5068	17842	30085	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus cuniculus sod gene
5470	18104	30423	3.56	3.0E-03	8922498.0	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5744	18370	31078	1.18	3.0E-03	AJ2488881.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5800	18434	31155	13.97	3.0E-03	U353223.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein Lmp22 (Lmp2) gene, complete cds
6870	19268	32070	10.41	3.0E-03	AA456701.1	EST_HUMAN	aa13101.1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7258	19784	32640	1.45	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pop3 gene for purine-cytosine permease
7551	20051	32624	3.37	3.0E-03	AB021736.1	EST_HUMAN	Oryza sativa gene for bzIP protein, complete cds
7879	20421	33239	0.91	3.0E-03	BF332058.1	EST_HUMAN	RC0-BT0812-250900-032-007 BT0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF332059.1	EST_HUMAN	RC0-BT0812-250900-032-007 BT0812 Homo sapiens cDNA
8097	20638	33549	4.71	3.0E-03	N82580.1	EST_HUMAN	2b27b04.51 Soares, parathyroid tumor NIH-PA Homo sapiens cDNA clone IMAGE:304783 3'
8257	20798		0.55	3.0E-03	M633498.1	NT	S.cerevisiae UGA35 gene, complete cds
8397	20837	33860	1.11	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNPA2A)
8419	20959	33977	1.31	3.0E-03	AL163268.2	NT	Home sapiens chromosome 21 segment HS21C0388
8522	21081		1.37	3.0E-03	CP901MB1	SWISSPROT	NONSTRUCTURAL PROTEIN V
8922	21460		12.62	3.0E-03	AW613774.1	EST_HUMAN	hs68p08x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:28891131 3' similar to contains L1.11 L1 repetitive element;
8976	21513	34346	4.44	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Table A

Table 4 Single Enzymes Expressed in Eetal Liver

Probe Seq ID	Exam Seq ID	ORF SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8899	21536	34466	6.98	3.0E-03	AI016731.1	EST_HUMAN	0x03d12x1 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1638247 3' similar to gb:X57138_mer1 HISTONE H2B.2 (HUMAN);	
9008	21545	34474	0.92	3.0E-03	BF338076.1	EST_HUMAN	602035880F1 NC1 CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183838 5'	
8830	21844		1	3.0E-03	D90091.1	NT	Synecdochesis sp. PCC8803 complete genome; 3/27, 271800-402288	
9368	20307	33210	0.68	3.0E-03	BE154870.1	EST_HUMAN	PM3-H10344-071288-003-007/H10344 Homo sapiens cDNA	
9554	22054		0.67	3.0E-03	P03355	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]	
8823	22123		5.92	3.0E-03	P08572	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	
9809	22307	35281	1.58	3.0E-03	P113089	SWISSPROT	RETRORVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	
8907	22404	35379	1.3	3.0E-03	P51889	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2A))	
10046	22541	35538	3.98	3.0E-03	AI163303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
10728	23254		4.28	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HE4B), mRNA	
11257	23787	38843	2.21	3.0E-03	AF002222.1	NT	Pneumocystis carinii kexin-like serine endopeptidase mRNA, partial cds	
11321	23019	38028	1.89	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GIP) gene, complete cds	
11354	23808	38887	3.86	3.0E-03	AF084481.1	NT	Homo sapiens tri nucleotide repeat DNA binding protein p20-CGGGBP (CGGGBP) gene, complete cds	
11354	23808	38888	3.98	3.0E-03	AF084481.1	NT	Homo sapiens tri nucleotide repeat DNA binding protein p20-CGGGBP (CGGGBP) gene, complete cds	
11707	24869		2.32	3.0E-03	AI525056.1	EST_HUMAN	prmtma-5.E07.7 bromaric Homo sapiens cDNA 5'	
11743	24142	36763	1.31	3.0E-03	AA983154.1	EST_HUMAN	07710.s1 Scores_total_fetus_NbzHF8_8W Homo sapiens cDNA clone IMAGE:1022779 3' similar to L1.13 MER26 repetitive element;	
11804	25007		1.81	3.0E-03	AB009888.1	NT	contains L1.13 MER26 repetitive element;	
11988	24298	30894	2.67	3.0E-03	AJ286282.1	NT	Homo sapiens gene for CMP-N-acetylneuraminate acid hydroxylase, partial cds	
541	13172	25651	0.8	2.0E-03	Q04652	SWISSPROT	Rattus norvegicus mRNA for connexin36 (cx36 gene)	
541	13172	25652	0.8	2.0E-03	QH4652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)	
818	15428		11.05	2.0E-03	T70874.1	EST_HUMAN	RING CANAL PROTEIN (KELCH PROTEIN)	
1407	14000	26529	2.25	2.0E-03	M20783.1	NT	ycf15n3.7 Scores fetal liver spleen INF5 Homo sapiens cDNA clone IMAGE:108341 5.	
1410	14003	26531	1.35	2.0E-03	AA861605.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7	
1418	14011	26540	20.98	2.0E-03	AF284446.1	NT	mu86101.s1 NC1 CGAP_Am1 Homo sapiens cDNA clone IMAGE:1217583	
1638	14128	26884	1.04	2.0E-03	P48509	SWISSPROT	Homo sapiens lamin-related protein DRC2 (DRC2) gene, complete cds	
1593	14155	26889	2.05	2.0E-03	4557888	NT	PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)	
1563	14165	26887	2.05	2.0E-03	4557888	NT	Homo sapiens procollagen-hsine, 2-oxoglutarate 5-dioxogenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA	
1635	14227		5.98	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPH-5(V) CHAIN PRECURSOR	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1807	14397	28942	1.01	2.0E-03 AA450138.1	EST_HUMAN	2x42a10_r1 Soares_total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:7891145	
1822	14607		0.89	2.0E-03 BE14908.1	EST_HUMAN	CM2-HT0183-061089-018-003 HT0183 Homo sapiens cDNA	
2038	14620	27183	1.25	2.0E-03 AF302689.1	NT	Mus musculus myelin expression factor 3-like protein gene, partial cds	
2291	14895	27440	0.97	2.0E-03 AL1633022.2	NT	Homo sapiens chromosome 21 segment HS2/C102	
2815	15777		4.13	2.0E-03 AW137782.1	EST_HUMAN	UI-H-811-ad1-9-10-0-U1_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:277170103'	
3463	16070	28543	4.95	2.0E-03 AA450138.1	EST_HUMAN	2x42a10_r1 Soares_total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:7891145	
3470	16076	28549	0.76	2.0E-03 BF568955.1	EST_HUMAN	60216386011 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:43000703'	
3729	16330	28796	6.87	2.0E-03 X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes	
4024	16622	28094	0.89	2.0E-03 AB046802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds	
4191	16780	28228	2.48	2.0E-03 P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GPR52; COAT PROTEIN GP38]	
4302	16898		12.85	2.0E-03 U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds	
4502	17086		1.08	2.0E-03 L35079.1	NT	Porcine rotavirus major outer capsid protein (VP77) mRNA, complete cds	
4518	17102		1.34	2.0E-03 AW297390.1	EST_HUMAN	U1-H-BW10-air-9-03-0-U1_s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:273204133'	
4523	17107	29553	0.98	2.0E-03 AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA	
4844	17226	28860	1.82	2.0E-03 L42512.1	NT	Drosophila melanogaster shortslighted class 2 (shs) mRNA, complete cds	
4844	17226	28881	1.82	2.0E-03 L42512.1	NT	Drosophila melanogaster shortslighted class 2 (shs) mRNA, complete cds	
4821	17389		1.92	2.0E-03 R87773.1	EST_HUMAN	yc45d02_s1 Soares_adult brain N2a-HB55Y Homo sapiens cDNA clone IMAGE:1808903'	
4848	17426	28878	5.2	2.0E-03 AA906468.1	EST_HUMAN	dh14f05_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:152234573'	
5167	17738	30163	0.81	2.0E-03 AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
5428	17985		0.9	2.0E-03 AF205067.1	NT	Desulfobrio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds	
5678	18305	30787	1.16	2.0E-03 BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:41048825'	
5810	24749	31158	2.28	2.0E-03 AB014583.1	NT	Xenopus laevis xifrin mRNA, complete cds	
5887	18510	31236	2.11	2.0E-03 U637711.1	NT	ATP-DEPENDENT NUCLEASE SUBUNIT B	
6258	18807	31636	4.06	2.0E-03 P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B	
6258	18887	31637	4.06	2.0E-03 P23477	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2)(CA-RP II)(CA-X)	
6486	19087	31869	2.38	2.0E-03 Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2)(CA-RP II)(CA-X)	
6486	19087	31870	2.38	2.0E-03 Q85203	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:41214085'	
6488	19089	31872	7	2.0E-03 BF308187.1	EST_HUMAN	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	
6521	19121	31912	2.17	2.0E-03 Q8UKP4	SWISSPROT	Lescutin mRNA for lysyl-tRNA synthetase (LysRS)	
6546	19144	31940	1.46	2.0E-03 X94451.1	NT		

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6715	18399			2.03	2.0E-03	AB991089.1	EST_HUMAN
7038	18958	30480	0.80	2.0E-03	AB038502.1	NT	wu36n09.x1 Scores_Dickteasee_cation_NH-CD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29_HUMAN P47814 60S RIBOSOMAL PROTEIN L29 :contains element MSR1 repetitive element ;Cennerhabditis elegans mRNA for gelsolin LEC-11, complete cds
7104	18974	32513	1.54	2.0E-03	5031884	NT	Homo sapiens lipoma HMGIC fusion partner (LHFPP) mRNA
7104	18974	32514	1.54	2.0E-03	5031884	NT	Homo sapiens lipoma HMGIC fusion partner (LHFPP) mRNA
7441	18521	32343	3.59	2.0E-03	BE067988.1	EST_HUMAN	CNA-BT0388-081269-054-d01 BT0388 Homo sapiens cDNA
7188	18728	32580	0.7	2.0E-03	AB288883.1	EST_HUMAN	qms6d11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1886885 3'
7335	18822	32726	0.87	2.0E-03	T88569.1	EST_HUMAN	yd77g10.1 Scores fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:14308 5'
7613	20128	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN)(LP)
7885	20337	33440	2.47	2.0E-03	AW592004.1	EST_HUMAN	h37b08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2894035 3' similar to TR:Q80976 Q80978 JERKY. ;
8159	20700	33814	5.98	2.0E-03	N20287.1	EST_HUMAN	yk42008.s1 Scores melanocyte 2N10HM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8159	20700	33815	5.98	2.0E-03	N20287.1	EST_HUMAN	yk42008.s1 Scores melanocyte 2N10HM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8208	20748	33982	0.62	2.0E-03	Q922350	SWISSPROT	HYPOTHETICAL_32kD PROTEIN C8G9.05 IN CHROMOSOME 1
8228	20789	33988	0.84	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005895	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005895	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU138679	EST_HUMAN	AU138679 PLACE1 Homo sapiens cDNA clone PLACE1004838 5'
8358	20898		2.04	2.0E-03	AJ400977.1	NT	Homo sapiens ASCL3 gene, CECF1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
9123	18598	31233	0.89	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
9123	18598	31234	0.69	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
9164	21699	34643	0.85	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9445	21971	34820	0.98	2.0E-03	H50832.1	EST_HUMAN	yp88e08.s1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:184288 3'
9477	21878	34823	2.57	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXBRACTION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (II) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-226) (TENASCIN-C) (TN-C)
9585	22036	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22036	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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96389 221389	35105	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds			
96389 221389	35106	0.54	2.0E-03 AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds		
98228 223277	35208	0.54	2.0E-03 AF097732.1	EST_HUMAN	QV3-0T0084-080400-144-001 OT0084 Homo sapiens cDNA		
98228 223277	35208	0.89	2.0E-03 AW864269.1	EST_HUMAN	2510a06.61 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE_894764 3'		
98228 223277	35208	4.55	2.0E-03 AA251376.1	EST_HUMAN	Human dystrophin gene		
10894 23415		3.24	2.0E-03 MB8524.1	NT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)		
11361 231283	33003	2.13	2.0E-03 P07354	SWISSPROT	RC3-BT0332-310800-115-g04 BT0332 Homo sapiens cDNA		
11417 238888		2.25	2.0E-03 BF330809.1	EST_HUMAN	H.sapiens variable number tandem repeat (VNTR) locus DNA		
11424 23875	368339	13.87	2.0E-03 Z11740.1	NT	Iy65n03.x1 NCI CGAP Kit11 Homo sapiens cDNA clone IMAGE_2283880 3' similar to SW:VATG_MANSE		
11687 24103		3.17	2.0E-03 AI825745.1	EST_HUMAN	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;		
11705 24118	37751	4.77	2.0E-03 AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds		
11730 24135	37755	1.94	2.0E-03 AI094325.1	EST_HUMAN	cy43q05.x1 Scerces_Jacchayoid tumor_NtH1PA Homo sapiens cDNA clone IMAGE_1688834 3' similar to TR:P07535 PS-PLA1 PRECURSOR. ;		
11754 18932		8.86	2.0E-03 AJ245167.1	NT	Camerus dromedarius chrp19 gene for immunoglobulin heavy chain variable region		
11897 25050		2.34	2.0E-03 AV697908.1	EST_HUMAN	AV697908 GCKC Homo sapiens cDNA clone GKCGX005 5'		
12062 24945	30984	1.49	2.0E-03 Y00598.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor		
12372 24542		2.08	2.0E-03 AF129758.1	NT	Home sapiens MSH5 gene, partial cds; and CLIC1, DDAH, G68, G8c, G8b, G8d, G8e, G8f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTb, TNF, and LTA genes, complete cds		
12551 24949		6.07	2.0E-03 AV687908.1	EST_HUMAN	AV697908 GCKC Homo sapiens cDNA clone GKCGX005 5'		
464 13098	25898	1.33	1.0E-03 HB8471.1	EST_HUMAN	y88c06.x1 Scerces_pineal gland_NSHFG Homo sapiens cDNA clone IMAGE_232334 5'		
882 13477	25902	1.47	1.0E-03 AI720283.1	EST_HUMAN	as70b08.x1 Barsteed codon HPLRB7 Homo sapiens cDNA clone IMAGE_2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENONYL-COA HYDRATASE. ;		
882 13477	25903	1.47	1.0E-03 AI720283.1	EST_HUMAN	as70b08.x1 Barsteed codon HPLRB7 Homo sapiens cDNA clone IMAGE_2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENONYL-COA HYDRATASE. ;		
1134 13737	26246	2.21	1.0E-03 AI885788.1	EST_HUMAN	wk88e08.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE_2422558 3'		
1154 13757	26267	1.31	1.0E-03 AI854572.1	EST_HUMAN	wk83e10.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE_2551242 3'		
1208 13098	26321	1.87	1.0E-03 AI892816.1	EST_HUMAN	wk86e01.x1 NCI CGAP_LU24 Homo sapiens cDNA clone IMAGE_2338440 3' similar to contains Alu repetitive element		
2074 14684	27227	4.05	1.0E-03 P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOCISIN I (HMWNII)		
2189 14775	27348	9.89	1.0E-03 AJ131018.1	NT	Homo sapiens SCL gene locus		
3008 15624	28102	1.45	1.0E-03 AB03117.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALLARY CARBONIC ANHYDRASE)		
3225 15837	28315	1.81	1.0E-03 P18915	SWISSPROT			

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							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3225	15837	28316	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3341	15851	28427	0.79	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3598	16200	28883	0.65	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3599	16200	28884	0.65	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3727	16328		1.31	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 xm63e07_x1 Score= NHCeC_cantek_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to
3897	16595	28067	0.75	1.0E-03	AW170552.1	EST_HUMAN	contains TAR1.1 TARI repetitive element;
4008	16603	28080	0.81	1.0E-03	Z48649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4528	17112	28568	4.29	1.0E-03	BE839162.1	EST_HUMAN	RC1-TN0128-160300-021-g01 TN0128 Homo sapiens cDNA
4574	17157	28601	5.77	1.0E-03	BE246538.1	EST_HUMAN	TCBAP1D4g09 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAp4g09
4770	17351	28863	0.83	1.0E-03	U28440.1	NT	Caenorhabditis elegans spliced leader RNA (SL4), and (SL5) genes
4850	17525	28898	2.83	1.0E-03	AI073485.1	EST_HUMAN	ov45c04_x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4850	17525	28897	2.83	1.0E-03	AI073485.1	EST_HUMAN	ov45c04_x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4851	17528		5.92	1.0E-03	BE154087.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5238	17800	30219	11.45	1.0E-03	O48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APOAIV)
5511	18144	30556	2.02	1.0E-03	AA290951.1	EST_HUMAN	Zs44f01.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5538	18228	30678	2.74	1.0E-03	AJ006345.1	NT	Homo sapiens Kv1.0T1 gene
5847	18275	30749	1.7	1.0E-03	KC03332.1	NT	Epstein-Barr virus (Ag378 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5847	18273	30750	1.7	1.0E-03	KC03332.1	NT	Epstein-Barr virus (Ag378 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5781	18387	31101	0.92	1.0E-03	BE708491.1	EST_HUMAN	601583841FT1NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943854 5'
5788	18382	31105	1.72	1.0E-03	Q02298	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6171	18763		2.62	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6209	18819	31590	1.1	1.0E-03	BE83939.2	EST_HUMAN	801657519R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3879883 3'
6339	18945		8.29	1.0E-03	11228178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1), mRNA
6476	19077	31860	1.21	1.0E-03	T87761.1	EST_HUMAN	yd83e11.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6541	19140		1.4	1.0E-03	AW902585.1	EST_HUMAN	QY3-NN1024-280400-171-005 NN1024 Homo sapiens cDNA
6852	18441	32258	1.31	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7206	18737	32590	2.48	1.0E-03	D16828.1	NT	Human gene for fourth somatostatin receptor subtype
7498	20021		1.72	1.0E-03	AJ228042.1	NT	Homo sapiens 858 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7835	20147	33030	1.7	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUISP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAK1), creatine transporter (CRT), CDM protein (CDM), atroventrikulodystrophy protein >

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7894	20203	33980	3.21	1.0E-03	M63376.1	NT	Human TRPM4-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE88044.1	EST_HUMAN	601481081F1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:38883278 5
7830	20172	33279	0.57	1.0E-03	AF274581.1	NT	Homo sapiens proctolin-releasing peptide receptor gene, 5' flanking region
7891	20433	33342	6.79	1.0E-03	AJ251973.1	NT	Homo sapiens partial stearin-1 gene
8080	20027	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	2697cd9e.s1 Soares_pregnant uterus_NbHPU_Homo sapiens cDNA clone IMAGE:4907683 3' similar to 2697cd9e.s1 Soares_pregnant uterus_NbHPU_Homo sapiens cDNA clone IMAGE:4907683 3' similar to contains L1_H1 L1 repetitive element;
8188	20777	33839	2.03	1.0E-03	AF153980.1	NT	Homo sapiens exostosis-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8389	20809	33828	0.81	1.0E-03	U28387.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21089	33888	0.52	1.0E-03	AA001613.1	EST_HUMAN	2182606.s1 Soares_fetal_liver_spleen_1NF1LS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21089	33889	0.52	1.0E-03	AA001613.1	EST_HUMAN	2182608.s1 Soares_fetal_liver_spleen_1NF1LS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V.cartari gene encoding volvoxopsin
8890	21438	34361	0.59	1.0E-03	AW640353.1	EST_HUMAN	CM3-LT0078-172020-092-007 LT0079 Homo sapiens cDNA
8009	21548			0.68	1.0E-03	U52111.2	NT
8047	21584	34514		3.37	1.0E-03	M30471.1	NT
8047	21584	34515		3.37	1.0E-03	M30471.1	NT
8525	22025	34882		1.98	1.0E-03	AF011400.1	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
8525	22025	34883		1.98	1.0E-03	AF011400.1	Thermotoga neapolitana alpha-1,6-galactosidase (sgdA) gene, complete cds
9734	22232	35210		0.94	1.0E-03	Q01129	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PC40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DPSG)
10068	22563	35558		0.57	1.0E-03	AF007485.1	NT
10073	22568			0.75	1.0E-03	AF007485.1	NT
10218	22713	35705		1.25	1.0E-03	AI024350.1	Human testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element;
10545	23082	36095		1.71	1.0E-03	AW3822393.1	EST_HUMAN
10545	23082	36096		1.71	1.0E-03	AW3822393.1	EST_HUMAN
10628	23161	36173		3.2	1.0E-03	BE170859.1	EST_HUMAN
10703	23232			3.19	1.0E-03	AI583847.1	EST_HUMAN
11036	23550			3.78	1.0E-03	AV759849.1	EST_HUMAN
11682	24098	37149		4.46	1.0E-03	BE894488.1	EST_HUMAN
12149	24392	30974		1.27	1.0E-03	9507208	NT

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12175	25030		5.89	1.0E-03	AI34755.1	EST_HUMAN	Ic05Fn11_x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains AU repetitive element.
12282	25052	30510	5.72	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
6862	18484		1.83	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-V PRECURSOR (APO-AIV)
6812	18209	32017	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
8561	22061		1.58	9.0E-04	ABC037203.1	NT	Glycyrhiza glabra GobAS1 mRNA for beta-emyrin synthase, complete cds
1635	14127		1.05	8.0E-04	X98468.1	NT	Xlaevis mRNA for CASR protein
4259	16845		5.17	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	28808	2.55	8.0E-04	U28185.1	NT	Homo sapiens phox protein (PPH) gene, complete cds
11024	23538		2.15	8.0E-04	AA777084.1	EST_HUMAN	zf24c10_s1 Soenes_fetal_heart_NBH119W Homo sapiens cDNA clone IMAGE:377874 3'
11175	23682		2.5	8.0E-04	AI571089.1	EST_HUMAN	in85608_x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2178310 3'
12500	24626	30892	1.85	8.0E-04	AW578894.1	EST_HUMAN	PM2-HT0353-130100-002-410 HT10353 Homo sapiens cDNA
1887	14453	27012	0.89	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2442	16009	27681	0.82	7.0E-04	U28186.1	NT	Homo sapiens pitrn protein (PPH) gene, complete cds
2739	15284	27861	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C1010
3319	15829	28408	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXorf6) mRNA
6248	18855	31626	0.75	7.0E-04	AA516212.1	EST_HUMAN	Ig65g12.21 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:339718 similar to contains L1_b3 L1 L1 repetitive element.
6836	19232		2.63	7.0E-04	AI786331.1	EST_HUMAN	wg36898_x1 Soenes_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
7279	19807		0.79	7.0E-04	AK02445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9719	22217	35191	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35192	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23890		3.42	7.0E-04	U78022.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44) and FTF3 (FTF3) genes, complete cds
11463	23913	36890	2.63	7.0E-04	Z40561.1	EST_HUMAN	HSC26A072 normalized infant brain cDNA Homo sapiens cDNA clone c-288a07 3'
12222	24443		11.57	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
12472	24597		4.94	7.0E-04	R17236.1	EST_HUMAN	y913c08_x1 Soenes Infant brain cDNA clone IMAGE:32288 5'
					8005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15278		0.83	6.0E-04	BF341380.1	EST_HUMAN	602013338F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149297 5'
4033	16831	28100	1.61	6.0E-04	A186225.1	EST_HUMAN	w156n11_x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	28205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29206	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4284	16850	28208	3.2	6.0E-04	U45693.1	NT	Homo sapiens CCR8 chemokine receptor (CCMR8) gene, complete cds
4538	17122	28557	0.83	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT10560 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4538 17122	28568	0.83	8.0E-04 BE172435.1	EST_HUMAN	RC2-HT0560-180200-011-409 HT0560 Homo sapiens cDNA		
5413 17970	30379	0.9	8.0E-04 AI806867.1	EST_HUMAN	RC-BT122-180389-057 BT122 Homo sapiens cDNA		
5413 17970	30380	0.9	8.0E-04 AI806867.1	EST_HUMAN	RC-BT122-180389-057 BT122 Homo sapiens cDNA		
7807 20550		3.04	8.0E-04 P48498	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)		
7858 20500		0.67	8.0E-04 H92847.1	EST_HUMAN	W84c11_s1 Soares_pineal_gland_NshPG Homo sapiens cDNA clone IMAGE:231858 3' similar to contains LOR1 repetitive element;		
8890 22387		3.74	8.0E-04 AL048607.2	EST_HUMAN	DKF2-586H2024-71 588 (synonym: hote1) Homo sapiens cDNA clone DKF2-586H2024		
8824 22420		0.77	8.0E-04 AI858286.1	EST_HUMAN	W35g02_s1 NCI_CGAP_Uri Homo sapiens cDNA clone IMAGE:2426830 3'		
8892 22487	35475	2.18	8.0E-04 BE00850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA		
10242 22737		0.64	8.0E-04 AF287476.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds		
11358 23812	36872	2.9	8.0E-04 AJ228042.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3		
11441 23861	36858	5.11	8.0E-04 AW013847.1	EST_HUMAN	UH-B10-88b-08-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'		
11445 23844		2.28	8.0E-04 Q101788	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-H2) (P18)		
118889 248288		3.55	8.0E-04 AW380518.1	EST_HUMAN	RC1-HT0269-281188-01-008 HT0269 Homo sapiens cDNA		
12871 24738		1.61	8.0E-04 AI817088.1	EST_HUMAN	W17g11_s1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;		
079 13303	25785	8.64	5.0E-04 O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF82)		
1549 14141		1.68	5.0E-04 AW851844.1	EST_HUMAN	QVD-CT0225-021098-030-007 CT0225 Homo sapiens cDNA		
3460 16087	28540	1.53	5.0E-04 AA548631.1	EST_HUMAN	nk27611_s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Ali repetitive element;		
3778 16378	28843	1.02	5.0E-04 Q9UKP4	SWISSPROT	ADAM-TS7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAM-TS7) (ADAM-TS7)		
5664 18261	30770	1.98	5.0E-04 AF248054.1	NT	Bos taurus microtumor calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds		
6740 18334	32141	6.37	5.0E-04 AA156080.1	EST_HUMAN	2033008_s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:5888633 5'		
7411 18336	32801	16.91	5.0E-04 M23804.1	NT	Genilla Gorilla involution gene medium allele, complete cds		
					qd13106_s1 Soares_plecanite_StdSeeks_2NbHP8ceW Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_scds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Ali repetitive element		
7898 20440	33348	4.97	5.0E-04 AI188382.1	EST_HUMAN	ob96802_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;		
8245 20788	33705	0.91	5.0E-04 AA814519.1	EST_HUMAN	EST_HUMAN		
8201 21718	34682	1.37	6.0E-04 AA846545.1	EST_HUMAN	bj59n03_s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1384357 3'		

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Probe Seq ID No:	Exon ID No:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	21883	34840	0.6	5.0E-04	NS3785.1	EST_HUMAN	KC2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KHC2745 5' similar to REPETITIVE ELEMENT
8437	21883	34912	0.65	5.0E-04	P28128	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE_XYLA PRECURSOR
8527	22027	34886	4.43	5.0E-04	AW270838.1	EST_HUMAN	X018602.1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10855	23376		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_71 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
11559	18291	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus microtender calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	18838	32801	1.84	5.0E-04	M23804.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
11809	24857		3.21	5.0E-04	AA568513.1	EST_HUMAN	inf15102.31 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U68834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
4115	13050		0.84	4.0E-04	BF241482.1	EST_HUMAN	6011876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	25810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	28012	1.48	4.0E-04	AI720283.1	EST_HUMAN	6870508.1x1 Barstestedt adam HPLB71 Homo sapiens cDNA clone IMAGE:2234039 3' similar to TR:Q13825
880	13494	28013	1.48	4.0E-04	AI720283.1	EST_HUMAN	Q13825 AL-BINDING PROTEIN/ENOL-COA HYDRATASE .
880	13494	28013	1.48	4.0E-04	AI720283.1	EST_HUMAN	6870508.1x1 Barstestedt adam HPLB71 Homo sapiens cDNA clone IMAGE:2234039 3' similar to TR:Q13825
1514	14108	28842	9.82	4.0E-04	AW753356.1	EST_HUMAN	RC3-CTD254-130100-023-f01 CT0254 Homo sapiens cDNA
2130	14708	27290	1.59	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0778
2179	14756		1.34	4.0E-04	AL045704.1	EST_HUMAN	DKFZp434D059_71 434 (synonym: hts43) Homo sapiens cDNA clone DKFZp434D059 5'
2858	15215	27797	1.83	4.0E-04	O98815	SWISSPROT	SERINCIN-2 (SILK GUM PROTEIN 2)
3200	15812	28286	2.59	4.0E-04	AF2811074.1	NT	Homo sapiens neuropilin 2 (NRFP2) gene, complete cds, alternatively spliced
3405	16014	28483	0.58	4.0E-04	AV8868624.1	EST_HUMAN	AV8868624 GKCH Homo sapiens cDNA clone GKCFH-H07 5'
3935	16533		0.94	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4415	17000	29442	3.2	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.51 NCI CGAP_C01 Homo sapiens cDNA clone IMAGE:3878910 5'
4416	17000	29443	3.2	4.0E-04	AA576331.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4635	17213	29571	1.94	4.0E-04	AA080324.1	EST_HUMAN	zn810108.81 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE:562670 3'
5249	17812	30225	8.04	4.0E-04	BE560680.1	EST_HUMAN	rh10a10.51 NCI CGAP_C01 Homo sapiens cDNA clone IMAGE:3878910 5'
7312	18840	32889	1.25	4.0E-04	IP48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7541	20081		2.42	4.0E-04	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
8473	21013	33829	1.42	4.0E-04	BF240712.1	EST_HUMAN	6011875835F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5'
8481	21020	33835	1.85	4.0E-04	N25507.1	EST_HUMAN	yx39er12.1x1 Saccharomyces melanocyte 2N-HM Homo sapiens cDNA clone IMAGE:2841425

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9898 22108	35070	2.79	4.0E-04	AI025689.1	EST_HUMAN	0x87f03.s1 Scores_ testis_NHT Homo sapiens cDNA clone IMAGE:184341 3'	
9754 22252		1.22	4.0E-04	AF02855.1	NT	Mus musculus neuropeptid-2(a17) mRNA, alternatively spliced, complete cds	
12188 246533		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced	
167 12830	25518	2.71	3.0E-04	AL119428.1	EST_HUMAN	DKF2p781J221_r1 781 (synonym: hmy2) Homo sapiens cDNA clone DKF2p781J221 5'	
208 12870	25558	3.63	3.0E-04	P49258	SWISSPROT	180 kD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2R)	
613 13528	26045	1.72	3.0E-04	U83891.1	NT	Human shn chain act4 Cox dehydrogenase gene, exons 1 and 2	
1870 14485	27022	5.5	3.0E-04	AI282100.1	EST_HUMAN	q28dc03.y1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028197 6'	
1884 14478		1.98	3.0E-04	AI898674.1	EST_HUMAN	th23q02x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'	
3348 15858	28434	4.85	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR	
4038 16834	29103	3.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)	
4131 16723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2	
4167 16758		1.14	3.0E-04	BE140098.1	EST_HUMAN	RCB-HT014-310589-028 HT0014 Homo sapiens cDNA	
4941 17516		5.05	3.0E-04	BE1531778.1	EST_HUMAN	PMQ-HT0339-180200-007-912 HT0339 Homo sapiens cDNA	
5162 17731	30158	0.57	3.0E-04	Q09472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300	
6292 18390		5.83	3.0E-04	AL162281.2	NT	Homo sapiens chromosome 21 segment HS21C081	
8909 19868	32295	1.87	3.0E-04	AL162278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
7660 20105	32881	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)	
8202 20743	33858	6.76	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	
9834 22232	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	ZX48d08.r1 Scores_ testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M627762	
10080 22375	35570	0.5	3.0E-04	AI892139.1	EST_HUMAN	VACUOULAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);	
10358 22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	WT75af11.x1 Scores_ thymus_NHT Homo sapiens cDNA clone IMAGE:1010490 similar to contains L1.12 L1	
11758 25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	nt24905.s1 Scores_ testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'	
12140 24909	30713	4.20	3.0E-04	AB018292.1	NT	RIbosomal PROTEIN L7A (HUMAN); repetitive element;	
12574 24871		3.54	3.0E-04	AL134483.1	EST_HUMAN	DKF2p547.186_r1 547 (synonym: mfr1) Homo sapiens cDNA clone DKF2p547.185 5'	
187 12848	25333	1.23	2.0E-04	AF217788.1	NT	Homo sapiens SCG31 like-protein, helicase-like protein NHL_M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds	
504 13138	25624	2.88	2.0E-04	AU146707.1	EST_HUMAN	AU146707HEMB1 Homo sapiens cDNA clone HEMBB1001253 3'	
840 13553	26068	5.4	2.0E-04	M88524.1	NT	Human dystrophin gene	
840 13553	26070	5.4	2.0E-04	M88524.1	NT	Human dystrophin gene	
1221 13821		3.94	2.0E-04	AI285021.1	EST_HUMAN	ch88e11.x1 Scores_ NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;	

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13827			1.85	2.0E-04 AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C0033
1872	14458			1.12	2.0E-04 AF224268.1	NT	Mus musculus 5' flanking region of Pit3 gene ZU35B05.51 Scores over tumor NbHOT Homo sapiens cDNA clone IMAGE:7403373 similar to contains AU repetitive element
2227	14802			0.9	2.0E-04 AA178860.1	EST_HUMAN	
2810	15172	27740		0.83	2.0E-04 U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV15S1P, TCRBV15S1A1T, HVB ratio, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TRY9, TRY10, TRY11, TCRBJ1S1, TCRBJ1S2; >
3016	15832	28109		1.13	2.0E-04 AI124528.1	EST_HUMAN	am58c08.X1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539780 3'
3377	15893	28484		0.78	2.0E-04	5174736	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16089	28581		2.53	2.0E-04 BE082317.1	EST_HUMAN	QV2BT0838-070500-194-b07 BT0838 Homo sapiens cDNA EST390590 MAGE sequences, MAGP Homo sapiens cDNA
3983	16581	29052		0.85	2.0E-04 AW979441.1	EST_HUMAN	EST390590 MAGP Homo sapiens cDNA
4224	16812			6.34	2.0E-04 U01029.1	NT	Phascolos vulgaris nitrate reductase (PNR2) gene, complete cds
4776	17357	28809		1.34	2.0E-04 H86265.1	EST_HUMAN	yu01e111r1 Scores_pineal gland_N23HPG_Homo sapiens cDNA clone IMAGE:232556 5'
4776	17357	28810		1.34	2.0E-04 H86265.1	EST_HUMAN	yu01e111r1 Scores_pineal gland_N23HPG_Homo sapiens cDNA clone IMAGE:232556 5'
4913	17488			1.79	2.0E-04 U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
6216	17780	30189		1.44	2.0E-04 AB037697.1	NT	Danio rerio hogaramo genes, exons 1 to 6, partial cds
5753	18359	31085		1.92	2.0E-04 AV654352.1	EST_HUMAN	AV654352 GLC_Homo sapiens cDNA clone GLCDUH10 3'
5745	18371	31078		1.87	2.0E-04 AI680862.1	EST_HUMAN	kp3b11.X1 NCI CGAP_UK3_Homo sapiens cDNA clone IMAGE:2207709 3'
6924	18546	31222		0.87	2.0E-04 AA286862.1	EST_HUMAN	EST11101 Uterus_Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470		1.06	2.0E-04 4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6335	18869	31769		0.81	2.0E-04 AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds, and unknown gene
7281	18629			2.44	2.0E-04 AU121712.1	EST_HUMAN	AU121712 MAMMA1_Homo sapiens cDNA clone MAMMA1000798 5'
7619	20129			13.03	2.0E-04 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7628	20138	33017		1.28	2.0E-04 P64288	SWISSPROT	MYOMESEN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33944		2.74	2.0E-04 U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33945		2.74	2.0E-04 U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8228	20767	33885		0.97	2.0E-04 AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8228	20767	33886		0.97	2.0E-04 AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33900		1.77	2.0E-04 AF020503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphate hydrolase (FH-TT) gene, exon 5

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8678 21217	34137	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)	
8257 21763	34138	0.47	2.0E-04	AA725700.1	EST_HUMAN	al22a12_s1 Soares testis_NCI Homo sapiens cDNA clone IMAGE:1343518 3'	
8340 21854	34803	0.5	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1	
8885 22382	35557	1.4	2.0E-04	BE148903.1	EST_HUMAN	RC3-HT0254-161089-011-b05 HT0254 Homo sapiens cDNA	
8890 22428	35490	2.39	2.0E-04	AA405777.1	EST_HUMAN	ZU68C11_1 Soares testis_NCI Homo sapiens cDNA clone IMAGE:742884 5'	
10731 23257	36273	6.22	2.0E-04	AV730373	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'	
11185 23890	36737	5.43	2.0E-04	AM40282.1	EST_HUMAN	#01f11_x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2140288 3' similar to contains Aliu repetitive element;	
11303 23798	36854	2.72	2.0E-04	AW138740.1	EST_HUMAN	UH-B11_adm-c-04-0-U1..s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'	
799 13416	25620	1.41	1.0E-04	H89846.1	EST_HUMAN	y28c09_s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2628864 3' similar to contains L111 L1 repetitive element;	
1113 13717	26227	2.57	1.0E-04	P11339	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	
1163 13756	26265	4.04	1.0E-04	AW013847.1	EST_HUMAN	U-H-B10_sub-e-09-0-U1..s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708826 3'	
1153 13759	26268	4.04	1.0E-04	AW013847.1	EST_HUMAN	U-H-B10_sub-e-09-0-U1..s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'	
1377 13970		3.85	1.0E-04	U62818.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds	
1689 14262	26785	2.57	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphotriesterformylchitamidine synthase, and LAMP (LAMP) genes, complete cds	
1689 14262	26786	2.57	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphotriesterformylchitamidine synthase, and LAMP (LAMP) genes, complete cds	
1901 14493	27047	2.44	1.0E-04	AB048942.1	NT	Equis caballus DNA_chromosome 24q14, microsatellite TKY38	
2711 152683	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	fm45cd8x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178388 3'	
2711 152683	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	fm45cd8x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178386 3'	
3323 158233	28410	1.1	1.0E-04	Q82203	SWISSPROT	SPLICEROSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A62)	
3799 18399	28864	2.7	1.0E-04	AM40282.1	EST_HUMAN	#01f11_x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2140288 3' similar to contains Aliu repetitive element;	
4134 16726	28180	1.72	1.0E-04	M14042.1	NT	Mouse epsilon 1 type IV collagen mRNA	
4158 16748	29201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLCBBDD04 3'	
5263 17825	30250	0.95	1.0E-04	AI357158.1	EST_HUMAN	q682h04-x1 NCI_CGAP_Ge4 Homo sapiens cDNA clone IMAGE:2005975 3'	
6021 18840	31380	1.5	1.0E-04	PO8547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
6568 19186	31982	0.97	1.0E-04	AA177111.1	EST_HUMAN	nc02e12_s1 NCI_CGAP_Pt3 Homo sapiens cDNA clone IMAGE:252	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	19594	32414	0.78	1.0E-04	AA564561.1	EST_HUMAN	hJ2804.31 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:3634883 similar to gp.M8/252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7237	19767	32623	14.09	1.0E-04	AI251880.1	EST_HUMAN	Q15710.11 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1885683 3'
7572	19767	32623	14.23	1.0E-04	AI251880.1	EST_HUMAN	Q15710.11 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1885683 3'
7837	20479	33389	1.02	1.0E-04	AA630433.1	EST_HUMAN	ab9498.31 Strategene lung (4837210) Homo sapiens cDNA clone IMAGE:854654 3'
8280	21786	34738	2.34	1.0E-04	AI805220.1	EST_HUMAN	W12608.1x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358742 3'
9270	21798	34745	1.71	1.0E-04	Q88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 6)
8348	21880		0.78	1.0E-04	TT7153.1	EST_HUMAN	jd72608.1x1 Scores fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
8584	22084	35023	2.2	1.0E-04	10883878	NT	Homo sapiens phosphotidylserine base 1 (PLSCR1), mRNA
10081	22578		2.87	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10116	22811	35681	0.83	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.06	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11503	23852	37020	1.88	1.0E-04	AB032988.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds
11540	23888	37050	2.1	1.0E-04	AW289081.1	EST_HUMAN	xy4912.1x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11570	24017	37086	1.87	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11570	24017	37087	1.87	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11670	24082		1.57	1.0E-04	BE87988.1	EST_HUMAN	CN0-CT0404-130700-476-H03 CT0404 Homo sapiens cDNA clone IMAGE:32860568 3' similar to contains L1.13 L1
11819	24878		1.98	1.0E-04	BE87938.1	EST_HUMAN	7728a10.1x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:32860568 3' similar to contains L1.13 L1 repetitive element;
727	13347	25839	1.93	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.1x1 Scores_NH3 Homo sapiens cDNA clone 12924688 3'
2047	14623	27198	0.92	9.0E-05	AW868218.1	EST_HUMAN	QV4-SN0023-070400-188-B04 SN0023 Homo sapiens cDNA
61117	18733	31488	1.45	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
83397	21820		2.71	9.0E-05	D85906.1	NT	Homo sapiens gene for cholecytokinin type-A receptor, complete cds
83398	21822	34771	2.79	9.0E-05	AF120882.1	NT	Homo sapiens methyl-CPG binding protein 1 (MBD1) gene, exon 15b
11017	23531	36587	2.86	9.0E-05	AW073078.1	EST_HUMAN	xy34g05.1x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:25887728 3' similar to contains L1.2 L1 repetitive element;
11121	23629	36671	1.88	9.0E-05	AI287878.1	EST_HUMAN	xy23t06.1x1 NCI_CGAP_Lyn8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
11483	18733	31488	3.89	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11874	24939		4.26	9.0E-05	AF128758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, Gab, Gcb, Gcd, Gab, Gcb, Gcd, Gcb, Gcb, Gcb, Gcb, Gcb, Gcb, Gcb, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
854	13470	25881	1.21	8.0E-05	AJ251848.1	NT	Plsum saithum mRNA for beta-1,3 glucanase (gns2 gene)
897	13511		9.89	8.0E-05	AJ251848.1	NT	Plsum saithum mRNA for beta-1,3 glucanase (gns2 gene)

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15583		0.71	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4570	17162	28604	1.87	8.0E-05	AW044605.1	EST_HUMAN	w778a04_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8883	21222	34142	0.49	8.0E-05	Y11688.1	NT	Mus musculus gene for nucleolinase II, exon 1 and joined CDS
11939	23544	39581	2.32	8.0E-05	M68197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12813	24621		2.72	8.0E-05	AA278333.1	EST_HUMAN	z588h01_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alt repetitive element; contains element MSR1 repetitive element;
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220388-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220388-011-E04 CT0208 Homo sapiens cDNA
583	13223	25697	3.82	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fetal cDNA Homo sapiens cDNA clone EST HFD072014
583	13223	25698	3.82	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fetal cDNA Homo sapiens cDNA clone EST HFD072014
1083	13698	28208	1.41	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15289	27885	3.67	7.0E-05	AL183278.2	NT	Human sapiens chromosome 21 segment HS21C0178
3184	15036	28279	4.68	7.0E-05	AB003080.1	NT	Dichotomium discoidatum gene for TRIFa, complete cds
4482	17048	28492	1.73	7.0E-05	AL183201.2	NT	Human sapiens chromosome 21 segment HS21C001
4543	17127	28570	0.58	7.0E-05	U63880.1	NT	Ceutorhynchus obliquus Stop1p homolog mRNA, complete cds
8167	20708	33824	1.11	7.0E-05	AA505582.1	EST_HUMAN	mb83g01_s1 NCI_CGAP_Br2_Homo sapiens cDNA clone IMAGE:9860098 3'
9472	21871	34820	3.74	7.0E-05	T07085.1	EST_HUMAN	EST04984 Fetal brain, Strategene (cat#836200) Homo sapiens cDNA clone HFBD60
11040	23554		7.95	7.0E-05	10835046	NT	Human sapiens sarcophyceen, epsilon (SGCE), mRNA
2073	14663	27225	2.03	8.0E-05	4885170	NT	Human sapiens chromosome X open reading frame 6 (CXorf6) mRNA
2073	14663	27226	2.03	8.0E-05	4885170	NT	Human sapiens chromosome X open reading frame 6 (CXorf6) mRNA
2624	15188	27753	1.34	8.0E-05	AI855241.1	EST_HUMAN	wb54h08_x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2308531 3' similar to gb:J03290 DNA TOPOISOMERASE I (HUMAN);
2709	152698	27833	0.9	8.0E-05	ZB4508.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC08a28B10
2709	152698	27834	0.9	8.0E-05	ZB4508.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC08a28B10
2840	13329	25815	2.88	8.0E-05	AF052630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5352	17912	30327	1.3	8.0E-05	AW8622309.1	EST_HUMAN	EST374382 MAGE resequences, MAGG Homo sapiens cDNA
6071	18898	31432	3.12	8.0E-05	Q12880	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6071	18898	31433	3.12	8.0E-05	Q12880	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31828	1.45	8.0E-05	N72828.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2462125
7013	18611	32332	0.79	8.0E-05	AA897880.1	EST_HUMAN	980a03_s1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8029	20571	33475	0.87	8.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141160-011-408 BT0311 Homo sapiens cDNA
8029	20571	33476	0.97	8.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141160-011-408 BT0311 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8381	20821	33841	0.85	6.0E-05 AA150482.1	EST_HUMAN	208208_x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:4817253 3' similar to contains element MEC228 repetitive element;	
8385	20825	33845	2.3	6.0E-05 AW886289.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA COMPLEMENT DEGRADATION FACTOR PRECURSOR	
8518	21055	33978	0.82	6.0E-05 Q80401	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)	
8178	21753	34689	1.09	6.0E-05 P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)	
9178	21753	34700	1.09	6.0E-05 P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)	
9440	21888	34915	1.13	6.0E-05 TB4140.1	EST_HUMAN	YE28c12_Tri Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:1190632 5'	
9837	22137	35103	0.57	6.0E-05 AW627985.1	EST_HUMAN	HS7403_x1 Scores_pregnant_Nb2HP Homo sapiens cDNA clone IMAGE:1425535 3' similar to contains Alt y88d08_x1 Scores_pregnant_Nb2HP Homo sapiens cDNA clone IMAGE:1425535 3' similar to contains Alt repetitive element; contains LTR7 repetitive element;	
10627	23159	36172	3.98	6.0E-05 R756339.1	EST_HUMAN	231580_x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:4870355	
11394	23846	36971	4.18	6.0E-05 AA044015.1	EST_HUMAN	2458702_x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA	
12183	24919	30718	10.28	6.0E-05 AW880110.1	EST_HUMAN	MRD-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA	
14489	14041	28559	18.37	5.0E-05 AW392086.1	EST_HUMAN	QV4-ST0234-2411984040-H11 ST0234 Homo sapiens cDNA	
1803	14488		1.76	6.0E-05 88223891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LCDC55895), mRNA	
40511	16848	28118	3.88	5.0E-05 AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1	
5716	18342	30848	11.28	5.0E-05 X58855.1	NT	Human MA Chm1 gene for embryonic myosin alkaline light chain, 3'UTR	
6144	18758	31518	2.87	6.0E-05 AV863544.1	EST_HUMAN	AV863544 GLC Homo sapiens cDNA clone GL-CDMA08 3'	
6316	18923	31700	0.97	5.0E-05 AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	
7370	18896		1.22	5.0E-05 AB031884.1	NT	Mus musculus gene for calretinin, exon 1	
11971	24460		5.73	5.0E-05 P49183	SWISSPROT	Homo sapiens TESTIN genes for calretinin, exon 1	
12249	24460		9.18	5.0E-05 P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)	
2833	12806		3.49	4.0E-05 U12821.1	NT	Human retin (REN) gene, 5' flanking region	
4580	17163	28605	1.37	4.0E-05 P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)	
4580	17163	28606	1.37	4.0E-05 P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)	
5166	17735	30162	0.58	4.0E-05 AF212313.1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds	
7020	18518	32340	0.75	4.0E-05 U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region	
8442	21988		7.28	4.0E-05 AF202835.1	NT	Homo sapiens PP1200 mRNA, complete cds	
8912	22408	35384	0.55	4.0E-05 P11369	SWISSPROT	RETOVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	
10305	22799	35790	0.73	4.0E-05 P23790	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)	
10648	23180	36193	5.05	4.0E-05 AW627984.1	EST_HUMAN	hs36c07_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;	
11850	24210	31041	3.27	4.0E-05 AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C32	
11929	24284		1.38	4.0E-05 AW117580.1	EST_HUMAN	xsfs36c08_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805182 3'	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	AJ248061.1	EST_HUMAN	q964c10_X1_Scenes_fetal_liver_spinec_INFEL_S1_Homo_sapiens_cDNA_clone IMAGE:1849458 3' similar to IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
1097	13702	28212	1.49	3.0E-05	AW273851.1	EST_HUMAN	NCBI-2814100 3'
1170	13772	28280	1.51	3.0E-05	BF037888.1	EST_HUMAN	601461463FT_NIH_MGC_88_Homo_sapiens_cDNA_clone IMAGE:3885142.5'
1170	13772	28281	1.51	3.0E-05	BF037888.1	EST_HUMAN	601461463FT_NIH_MGC_88_Homo_sapiens_cDNA_clone IMAGE:3885142.5'
2746	15301	27887	1.17	3.0E-05	Q62234	SWISSPROT	SKELEMIN
3331	15641		0.69	3.0E-05	AJ288919.1	EST_HUMAN	Q91g11_X1_Scenes_NHNMPU_S1_Homo_sapiens_cDNA_clone IMAGE:1870748 3' similar to TR:008632
4471	17057	28503	7.22	3.0E-05	BE168211.1	EST_HUMAN	PM1-HT0521-120203-001-e10 HT0521_Homo_sapiens_cDNA
4471	17057	28504	7.22	3.0E-05	BE168211.1	EST_HUMAN	PM1-HT0521-120203-001-e10 HT0521_Homo_sapiens_cDNA
4585	17148	28594	1.08	3.0E-05	AA388678.1	EST_HUMAN	EST779898_Placenta_I_Homo_sapiens_cDNA_similar to similar to p53-associated protein
4585	17148	28595	1.08	3.0E-05	AA388678.1	EST_HUMAN	EST779898_Placenta_I_Homo_sapiens_cDNA_similar to similar to p53-associated protein
4692	17274		0.71	3.0E-05	AL1633022	NT	Homo_sapiens_chromosome_21_segment_HS21C102
4726	17307	28751	0.75	3.0E-05	AF149773.1	NT	Homo_sapiens_NOD1_protein (NOD1) gene, exons 1, 2, and 3
4863	13330	25817	0.65	3.0E-05	AJ248061.1	EST_HUMAN	q964c10_X1_Scenes_fetal_liver_spinec_INFEL_S1_Homo_sapiens_cDNA_clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
5746	18372	31080	1.73	3.0E-05	11072102	NT	Mus_musculus_myostatin_light_chain_2_precursor_lymphocyte-specific (Myo2p), mRNA
6854	19442	32257	1.28	3.0E-05	AJ225782.1	NT	Homo_sapiens_SYBL1_gene, exons 6-8
6854	19442	32258	1.28	3.0E-05	AJ225782.1	NT	Homo_sapiens_SYBL1_gene, exons 6-8
7839	20381	33288	1.9	3.0E-05	BE738157.1	EST_HUMAN	601567451FT_NIH_MGC_21_Homo_sapiens_cDNA_clone IMAGE:38472292.5'
8283	20834	33756	1.29	3.0E-05	AA284049.1	EST_HUMAN	ZG60055.1 Stratagene schizo brain S11_Homo_sapiens_cDNA_clone IMAGE:701841 3'
8824	21363	34288	1.78	3.0E-05	AW770882.1	EST_HUMAN	HB14608_X1_NCI_CGAP_Lu24_Homo_sapiens_cDNA_clone IMAGE:3008638 3'
8828	21387	34291	1.22	3.0E-05	6912431	NT	Homo_sapiens_Interleukin-1_receptor_antagonist_homolog_1 (IL1HY1), mRNA
8832	21371	34286	0.47	3.0E-05	P433801	SWISSPROT	MELANOMA-ASSOCIATED_ANTIGEN_8 (MAGE-8 ANTIGEN)
9058	21585		0.88	3.0E-05	X03273.1	NT	Human Alu-family cluster 5 of alpha(1)-acid glycoprotein gene
8244	21770	34718	1.3	3.0E-05	AA372562.1	EST_HUMAN	EST84475_Colon_adenocarcinoma_IV_Homo_sapiens_cDNA_5' end
8581	22081		2.97	3.0E-05	AI76831.1	EST_HUMAN	W536R9_X1_Scenes_NSF_F8_9W_OT_PA_P_S1_Homo_sapiens_cDNA_clone IMAGE:2387209 3'
10428	22822	35925	0.85	3.0E-05	Q62818	SWISSPROT	PROTEIN_KINASE_C-BINDING_PROTEIN_NEU2_PRECURSOR (NEU-LIKE PROTEIN 2)
10428	22822	35928	0.85	3.0E-05	Q62818	SWISSPROT	PROTEIN_KINASE_C-BINDING_PROTEIN_NEU2_PRECURSOR (NEU-LIKE PROTEIN 2)
12055	24338		1.48	3.0E-05	AJ271735.1	NT	Homo_sapiens_Xq_pseudoautosomal_region_segment_1/2
12387	25101		1.52	3.0E-05	AW518889.1	EST_HUMAN	xs88d68_X1_Scenes_NFL_T_GCB_S1_Homo_sapiens_cDNA_clone IMAGE:2776811 3'
2262	14633	27506	1.55	2.0E-05	AI286621.1	EST_HUMAN	q98e11_X1_Scenes_NFL_T_GCB_S1_Homo_sapiens_cDNA_clone IMAGE:1855052 3' similar to contains MER3_b2 MER3 repetitive element;
2619	15181	27747	10.28	2.0E-05	M137922.1	NT	Human adenosine deaminase (ADA) gene, complete cds

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2798	15233		6.73	2.0E-05 AA160562.1	EST_HUMAN	xp46a12.1f Strategene NNT neuron (#8372233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;	
3171	15785	28257	1.59	2.0E-05 BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA	
3391	15889	28477	0.63	2.0E-05 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
3416	16024	28508	1.04	2.0E-05 X089211.1	NT	H. sapiens DNA for endogenous retroviral like element	
3541	16149		0.72	2.0E-05 X05465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV	
3880	16473		0.67	2.0E-05 AL039107.1	EST_HUMAN	DKFZp569I084_11 568 (synonym: hkd2) Homo sapiens cDNA clone DKFZp569I084 5'	
5010	17583	30028	0.63	2.0E-05 AJ131016.1	NT	Homo sapiens SCL gene locus	
5176	17743		2.42	2.0E-05 LT77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end	
5633	18555	31282	1.84	2.0E-05 AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	
6125	18740	31482	1.4	2.0E-05 Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+))DICARBOXYLATE COTRANSPORTER	
6125	18740	31483	1.4	2.0E-05 Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+))DICARBOXYLATE COTRANSPORTER	
6305	18912	31686	0.73	2.0E-05 AI140272.1	EST_HUMAN	cc72a02_x1 Scores_placenta_8to9weeks_2hIP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'	
6738	18330	32138	2.12	2.0E-05 AA714330.1	EST_HUMAN	similarity to contains L1,13 L1 repetitive element;	
6882	19480	32301	2.2	2.0E-05 Y08926.1	NT	rm08d12.6 NCI_CGAP_SST1 Homo sapiens cDNA clone IMAGE:12388519 3'	
6894	19492	32313	1.94	2.0E-05 AI492890.1	EST_HUMAN	P_fabipurum mRNA for AARP1 protein, partial	
7002	18500		8.08	2.0E-05 AB991025.1	EST_HUMAN	Q247D08_x1 NCI CGAP_KR11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711	
7207	19738	32501	2.2	2.0E-05 AF224282.1	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN:	
7207	19738	32502	2.2	2.0E-05 AF224282.1	NT	W035H07_x1 Scores_Dickegraeber NHCD Homo sapiens cDNA clone IMAGE:2522077.3'	
7403	18923		0.91	2.0E-05 AF128947.1	NT	Heterodotius brasiliensis HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA8 (HoxA8), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	
7828	20368	33270	1.41	2.0E-05 A1381040.1	EST_HUMAN	Heterodotius brasiliensis HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA8 (HoxA8), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	
9101	21708	34651	0.49	2.0E-05 P49457	SWISSPROT	q2020h05_x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108389 3'	
9101	21708	34652	0.49	2.0E-05 P49457	SWISSPROT	COMPLEMENT DEGRADATION-ACCELERATING FACTOR (CD55)	
9837	22335	35317	0.48	2.0E-05 AL163207.2	NT	COMPLEMENT DEGRADATION-ACCELERATING FACTOR (CD55)	
10041	22538	35532	0.74	2.0E-05 BF055639.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007	
							7175g09_y1 NCI CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340578 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10482	22878	35884	2.62	2.0E-05	NA1751.1	EST_HUMAN	yw91ac03.1 Soares_placenta_8to9weeks_201HIPatGW Homo sapiens cDNA clone IMAGE:256970_5'
10482	22878	35885	2.62	2.0E-05	NA1751.1	EST_HUMAN	yw91ac03.1 Soares_placenta_8to9weeks_201HIPatGW Homo sapiens cDNA clone IMAGE:256970_5'
10524	18500		2.44	2.0E-05	AI891025.1	EST_HUMAN	w425f07.1x1 Soares_Dictyostelium_catenatum_NHOD_Homo sapiens cDNA clone IMAGE:2522077_3'
111327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RCS-HTT0582-28030042-E12-HTT0582 Homo sapiens cDNA
11883	24644		4.81	2.0E-05	BE346229.1	EST_HUMAN	Inv21802.1x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532_3' similar to TR.Q12832
12680	25018		13.02	2.0E-05	AW074604.1	EST_HUMAN	x886a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932_3' similar to contains L1.1s L1 repetitive element;
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12855	24727		2.35	2.0E-05	AI200970.1	EST_HUMAN	qf88g11.1x1 Soares_leptospermum_leptospermum_NHT Homo sapiens cDNA clone IMAGE:1755298_3'
2719	15475	27841	1.45	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment Lsmtb_120 Suppressor of Hairyless (Su(H)) gene, partial cds
3711	16812	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lsmtb_120 Suppressor of Hairyless (Su(H)) gene, partial cds
40339	168337	28105	11.8	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LCN
4252	168440	28289	0.88	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4384	168511	28391	1.89	1.0E-05	AA43119.1	EST_HUMAN	zv468g01.1x1 Soares_leptocheilus_leptocheilus_NHT Homo sapiens cDNA clone IMAGE:781494_5'
4876	17550	28892	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy48g11.1x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548_3'
5395	17853		0.94	1.0E-05	AI733568.1	EST_HUMAN	ce84d07.x6 NCI_CGAP_Bi2 Homo sapiens cDNA clone IMAGE:1610125_3' similar to contains Altu repetitive element;
5420	17853	30369	0.91	1.0E-05	L27585.1	NT	Mus musculus bradykinin B2 receptor (B2R) gene, complete cds
6848	18438	32252	1.32	1.0E-05	AJ248003.1	NT	Homo sapiens Spast gene for spastic protein
7140	18620	32342	3.98	1.0E-05	AA841946.1	EST_HUMAN	re19g22.61 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114_3' similar to contains L1.M L1 L1 repetitive element;
7142	18675	32515	14.32	1.0E-05	4505844	NT	Homo sapiens phosphodiesterase A2, group X (PLA2G10) mRNA, and translated products
7655	20167	33054	0.76	1.0E-05	BF222848.1	EST_HUMAN	Tp57f01.1x1 NCI_CGAP_P-28 Homo sapiens cDNA clone IMAGE:3649945_3' similar to contains MER10.x3 MER10 repetitive element;
7754	20262		2.22	1.0E-05	P1974	SWISSPROT	S2 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8848	21385		2.58	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8890	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	zg35h12.31 Soares_total_fetus_NH2HF8_9w Homo sapiens cDNA clone IMAGE:788519_3' similar to gb:J02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
8211	21728	34671	13.74	1.0E-05	AA236110.1	EST_HUMAN	zg56f11.1x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332_5' similar to contains Altu repetitive element; contains element TAR1 repetitive element ;
9288	21688	34834	0.6	1.0E-05	AV732190	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFB1H01_5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9752	22290	35232	0.76	1.0E-05	AW510802.1	EST_HUMAN	hd41b02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR_H1 OFR repetitive element;
9752	22290	35233	0.76	1.0E-05	AW510802.1	EST_HUMAN	hd41b02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR_H1 OFR repetitive element;
9830	22329	35209	1.58	1.0E-05	AW281521.1	EST_HUMAN	U+H-B12_89k-08-0-UJ_81 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9830	22329	35310	1.58	1.0E-05	AW281521.1	EST_HUMAN	U+H-B12_89k-08-0-UJ_81 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10087	22532		1.73	1.0E-05	AW488885.1	EST_HUMAN	hd07c10_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L112 L1 repetitive element;
10789	23322	36832	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorC gene, and sodium phosphate transporter (NPT3) gene, complete cds
10789	23322	36833	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorC gene, and sodium phosphate transporter (NPT3) gene, complete cds
12483	25011	30616	1.67	1.0E-05	AL103303.2	NT	Homo sapiens chromosome 21 segment HS21/C103
2696	15253	27824	4.74	9.0E-06	AI583811.1	EST_HUMAN	nt73d08_x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248388 3'
3130	15744	28213	5.23	9.0E-06	AI218883.1	EST_HUMAN	cg11008_x1 Soares_placenta_8to9weeks_2N1H-IP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
3670	16271		3.37	9.0E-06	M6775.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
60034	18681	31423	2.25	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD230 gene, exons 5, 6
6947	18524	32346	0.84	9.0E-06	BE05042.1	EST_HUMAN	RC1-BT023-1410500-017-a07 BT0313 Homo sapiens cDNA
7468	18888	32653	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE_HOMOLOG
7751	20259	33193	12.47	9.0E-06	AI034270.1	EST_HUMAN	ox2dg01_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1859912 3' similar to contains Alu repetitive element;
8400	20940	33883	1.18	9.0E-06	AI103298.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21451	34372	2.48	9.0E-06	Q63788	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V_SRC)
8913	21451	34373	2.48	9.0E-06	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V_SRC)
9149	21684	34628	4.8	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10618	23339	36353	3.70	9.0E-06	Q10384	SWISSPROT	PUTATIVE SERINE/TREONINE-PROTEIN KINASE C22E12.14G
2589	15469	27701	1.48	8.0E-06	AW382538.1	EST_HUMAN	RC3-CT0283-201188-011-h11 C10283 Homo sapiens cDNA
10424	22918	35919	0.84	8.0E-06	P340883	SWISSPROT	FASCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22918	35820	0.84	8.0E-06	P340883	SWISSPROT	FASCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1015	13625		1.71	7.0E-06 AA689728.1	EST_HUMAN		ab8010.51 Strategene lung (A837720) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.1 MER20 repetitive element;
1487	14080	26919	3.38	7.0E-06	7682177 NT		Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2177	14754	27324	1.55	7.0E-06 AW583215.1	EST_HUMAN		hg11b12-x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845278 3' similar to sp:XB2048_cds1 WE1-LIKE PROTEIN KINASE (HUMAN);
2897	15514		7.94	7.0E-06 A1388252.1	EST_HUMAN		gnl:6039_x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1897288 3' similar to contains Alu repetitive element.
3620	16223		1	7.0E-06 AA385542.1	EST_HUMAN		EST88205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5874	18488		5.81	7.0E-06 AW883141.1	EST_HUMAN		QV2-O70062-250400-173-H01 O70062 Homo sapiens cDNA
5972	18583	31327	0.84	7.0E-06 N98845.1	EST_HUMAN		Y85c07_x1 Soares_multiple_sclerosis_2NBHNSP Homo sapiens cDNA clone IMAGE:278412 5'
6724	21283	34183	0.72	7.0E-06	11420709 NT		Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXf68S1E), mRNA
8814	22312		2.32	7.0E-06 Q61147	SWISSPROT		CERULOPLASMIN PRECURSOR (FEROXIDASE)
11710	25043	30508	1.62	7.0E-06 BF215972.1	EST_HUMAN		801881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2842	15558	28032	1.29	6.0E-08 BE068189.1	EST_HUMAN		QV3-BT0378-010300-105-011 B10378 Homo sapiens cDNA
4885	16894	28085	2.03	6.0E-08 Q01498	SWISSPROT		OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4875	17450	28901	1.47	6.0E-08 AI840989.1	EST_HUMAN		ox08602_x1 Soares_fetal_liver_sapien_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
56552	18184	30569	1.3	6.0E-08 AF187441.1	NT		Mus musculus E-cadherin binding protein E7 mRNA, complete cds
56905	18234	30885	1.15	6.0E-08 Q92240	SWISSPROT		PROTEIN XE7
9770	22268		1.67	6.0E-08 AW801612.1	EST_HUMAN		IL6-JM070-110400-063-g02 U1M070 Homo sapiens cDNA
12802	244888	30881	1.47	6.0E-08	11418157 NT		Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
53861	17821	30335	1.02	5.0E-09 AL183288.2	NT		Homo sapiens chromosome 21 segment HS21_2088
6211	18821	31592	3.73	5.0E-08 AL183246.2	NT		Homo sapiens chromosome 21 segment HS21_0048
6479	18080	31863	2.04	5.0E-08 U07561.1	NT		Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7284	18812	32868	1.11	5.0E-08 AB007548.1	NT		Homo sapiens gene for LECT2, complete cds
10013	22508	35498	6.57	5.0E-08 AA313620.1	EST_HUMAN		EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10406	22800	35895	0.54	5.0E-08 P06881	SWISSPROT		COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12482	24616	30890	13.8	5.0E-08 AID85045.1	EST_HUMAN		HA9877 Human fetal liver cDNA library Homo sapiens cDNA
675	13299	25780	6.05	4.0E-08 R18267.1	EST_HUMAN		ye48cc03_x1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element;contains element MER21 repetitive element;
878	13493	26011	6.94	4.0E-08 AW103354.1	EST_HUMAN		xc68g12_x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:288957 3' similar to contains Alu repetitive element;contains element MER21 repetitive element;

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379 13972	28499		3.92	4.0E-06	A1334828.1	EST_HUMAN	hs33e05_x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2058168 3'
1379 13972	28500		3.92	4.0E-06	A1334828.1	EST_HUMAN	hs33e05_x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2058168 3'
1522 14114	28851		3.17	4.0E-06	BF385812.1	EST_HUMAN	OY2-NT0046-200800-250-H07 NT0046 Homo sapiens cDNA
2305 14878	27454		1.89	4.0E-06	AW016401.1	EST_HUMAN	U1-H-B10-est4-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:271025 3'
3098 15714	28186		1.26	4.0E-06	AF98348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3983 16561	28030		1.35	4.0E-06	AW848285.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA clone IMAGE:2132562 3' similar to contains element
4830 17505	28851		1.88	4.0E-06	A1886839.1	EST_HUMAN	wiBac10_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2132562 3' similar to contains element
5053 17826	30070		2.12	4.0E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8438 20878	33890		0.53	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE_SERINE 2
8735 21274	34195		2.68	4.0E-06	AF008690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV12S2 region
9824 22124	35098		1.11	4.0E-06	A1272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11324 230222	36031		3.84	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
2208 14784	27357		1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08_s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1_t1 L1 repetitive element;
2208 14784	27358		1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08_s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1_t1 L1 repetitive element;
2307 14879			1.54	3.0E-06	AF202835.1	NT	Homo sapiens PPI200 mRNA, complete cds
2948 15584	28038		1.02	3.0E-06	AA888218.1	EST_HUMAN	ak48g11_s1 Soares_NHT Homo sapiens cDNA clone IMAGE:1408232 3' similar to contains LTR1.13
3304 15915			2.41	3.0E-06	A857778.1	EST_HUMAN	W22405_x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR-080734 080734
3851 16449	28971		1.08	3.0E-06	BE047094.1	EST_HUMAN	LINE-1 LIKE PROTEIN :contains L1_t2 L1 repetitive element;
3851 16449	28972		1.08	3.0E-06	BE047094.1	EST_HUMAN	hg84d12_x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4573 17158	28860		0.68	3.0E-06	T50288.1	EST_HUMAN	hg84d12_x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4861 17243	28897		4.82	3.0E-06	X54816.1	NT	hg84d10.1 Strategene ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
5045 17618	30053		0.94	3.0E-06	J04033.1	NT	Homo sapiens gene for alpha-1-microglobulin-beta-kunitin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
5045 17618	30064		0.94	3.0E-06	J04033.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
6308 18915	31689		0.78	3.0E-06	AU158412	EST_HUMAN	AU158412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7280 18808			2.79	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8027 20569	33473		0.72	3.0E-06	BE562864.1	EST_HUMAN	601332125f1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3860314 5'
8618 21157	34070		0.69	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12162	24384			13.37	3.0E-08 AW385262.1	EST_HUMAN	RC0-LT0001-2611889-011-A03 LT0001 Homo sapiens cDNA HOMEBOX PROTEIN GOOSECOLD
216	12877			2.91	2.0E-08 P54300	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1614	14207			4.46	2.0E-08 P21414	SWISSPROT	
					ws04e03_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30 b1		
2418	14988	27580	2.2	2.0E-08 AI672138.1	EST_HUMAN		MER30 repetitive element;
2506	15070	27643	1.79	2.0E-08 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	
2891	15163	27731	1.34	2.0E-08 P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)	
3570	16174	29856	1.04	2.0E-08 AV657555	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'	
3825	16425	28887	1.85	2.0E-08 AA173518.1	EST_HUMAN	2P02605_11 Stratagene ovarian cancer (#837119) Homo sapiens cDNA clone IMAGE:3895232 5'	
3838	16435	28897	0.83	2.0E-08 AW450215.1	EST_HUMAN	UH-BR_dlyg-0-01_U.1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'	
3844	16443	28904	1.74	2.0E-08 AB030886.1	NT	Mus musculus gene for odorant receptor A18, complete cds	
6239	18248		0.78	2.0E-08 AA1974832.1	EST_HUMAN	cn34h01_s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1553869 3' similar to contains Ali repetitive element;	
6267	18375	31643	0.87	2.0E-08 AI539448.1	EST_HUMAN	ls6f105_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR-Q13537	
6570	19168	31985	4.94	2.0E-08 AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE .;	
7858	20400		0.89	2.0E-08 AW889223.1	EST_HUMAN	wf80004_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410683 3'	
8033	20575	33480	0.75	2.0E-08 T12238.1	EST_HUMAN	MR3-SR0087-12040-002-f02 SN0087 Homo sapiens cDNA	
8770	21309		0.59	2.0E-08 AA772497.1	EST_HUMAN	A44TR_H-Heart Homo sapiens cDNA clone A447 zh27c11_s1 Soares_joined_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR-P70467 P70467 REVERSE TRANSCRIPTASE ;	
8782	21321	34245	1.54	2.0E-08 H62031.1	EST_HUMAN	y437G04_11 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:2355074 5' similar to gb:X74929	
9143	21678	34621	0.91	2.0E-08 AF003529.1	NT	KERATIN, TYPE II CYTOSKELETON 8 (HUMAN); Homo sapiens glycopin 3 (GPC3) gene, partial cds and flanking repeat regions	
9143	21678	34622	0.91	2.0E-08 AF003529.1	NT	Homo sapiens glycopin 3 (GPC3) gene, partial cds and flanking repeat regions	
9817	22117	35080	0.72	2.0E-08 N30578.1	EST_HUMAN	ym686d03_s1 Soares_placenta_8to9weeks_2NB-IPstew8W Homo sapiens cDNA clone IMAGE:257212 3'	
9833	22331		0.63	2.0E-08 AV748989.1	EST_HUMAN	AV748989 NPC Homo sapiens cDNA clone NPCAXD05 5'	
12052	25048	30508	1.61	2.0E-08 P23249	SWISSPROT	PROTEIN M0V-10	
12210	24434		6.63	2.0E-08 BE328232.1	EST_HUMAN	hs9202_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144689 3' similar to contains L112 L1 repetitive element;	
38	12715	26174	1.77	1.0E-08 O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)	
885	13309	25704	1.45	1.0E-08 AF084384.1	NT	Mus musculus D8M45E protein (DBM45E) mRNA, complete cds	
1500	14092	26831	2.08	1.0E-08 P09125	SWISSPROT	MEROZITE SURFACE PROTEIN CMZ-8	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1571	14164	28895	1.12	1.0E-08 AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C0378	
1627	14220		1.54	1.0E-08 P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT	
2037	14619	27183	8.38	1.0E-08 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
2037	14619	27187	8.38	1.0E-08 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
4459	17045	28488	14.7	1.0E-08 U07561.1	NT	Human ABL gene, exon 16 and intron 1b, and putative M6804 Met protein (M6804 Met) gene, complete cds	
5269	17831	30256	0.98	1.0E-08 AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C0385	
5269	17831	30257	0.99	1.0E-08 AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C0385	
6494	18128	30533	4.64	1.0E-08 BF332015.1	EST_HUMAN	MR1-BT0800-030700-002-008 BT0800 Homo sapiens cDNA	
5518	18150	30583	1.08	1.0E-08 BE834518.1	EST_HUMAN	MR3-FN0004-050800-001-004 FN0004 Homo sapiens cDNA	
5518	18150	30584	1.08	1.0E-08 BE834518.1	EST_HUMAN	MR3-FN0004-050800-001-004 FN0004 Homo sapiens cDNA	
5687	18294	30774	1.13	1.0E-08 CG0813	SWISSPROT	15 kDa SELENOPROTEIN PRECURSOR	
6954	18631	32358	5.98	1.0E-08 P02871	SWISSPROT	FIBRINOGEN ALPHA-E CHAIN PRECURSOR	
7043	20486		0.68	1.0E-08 AA912623.1	EST_HUMAN	c23c08_s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1624878 3'	
8218	20757	33671	1.21	1.0E-08 AI47010.1	EST_HUMAN	qp54e022_x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1928842 3'	
8425	20985	33879	1.23	1.0E-08 AI287878.1	EST_HUMAN	q123n08_x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;	
9228	21950	34889	0.98	1.0E-08 N74695.1	EST_HUMAN	ze55e01_s1 Scores_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'	
9330	21901	34850	0.5	1.0E-08 Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	
9630	22100	35082	3.34	1.0E-08 US28688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds	
9630	22100	35083	3.34	1.0E-08 US28688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds	
9843	22143	35111	4.38	1.0E-08 AA132611.1	EST_HUMAN	z017608_r1 Strategene clone (#837204) Homo sapiens cDNA clone IMAGE:587174 5'	
9703	22202		3.84	1.0E-08 AA440257.1	EST_HUMAN	z04d11_s1 Scores_Mat_fetus_Nb21IF8_8w Homo sapiens cDNA clone IMAGE:785403 3' similar to qb:D28328 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);	
10382	22876		1.61	1.0E-08 AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C033	
11502	23951		6.24	1.0E-08 AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-003 NT0054 Homo sapiens cDNA	
12087	24358	30863	7.83	1.0E-08 L78810.1	NT	Homo sapiens ADP//ATP carrier protein (ANT-2) gene, complete cds	
12185	14619	27183	1.67	1.0E-08 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
12185	14619	27187	1.67	1.0E-08 AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
12803	14220		1.38	1.0E-08 P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT	
383	13030	25518	2.01	9.0E-07 AF00528.1	NT	Homo sapiens Giphcan 3 (GPC3) gene, partial cds and flanking repeat regions	
383	13030	25519	2.01	9.0E-07 AF00529.1	NT	Homo sapiens Giphcan 3 (GPC3) gene, partial cds and flanking repeat regions	
8246	20887		0.57	9.0E-07 AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C0380	
11128	23634	30675	2.86	9.0E-07 AL183281.2	NT	Homo sapiens chromosome 21 segment HS21C0381	

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Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885 17460	238112	5.02	8.0E-07 AI288598.1	EST_HUMAN	q182g07_x1_Soares_NIHMPU_S1	Homo sapiens cDNA clone IMAGE:1878878 3'	
4885 17460	238113	5.02	8.0E-07 AI288598.1	EST_HUMAN	q182g07_x1_Soares_NIHMPU_S1	Homo sapiens cDNA clone IMAGE:1878878 3'	
6047 186688		7.49	8.0E-07 P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]		
7944 20486		9.51	8.0E-07 AF135416.1	NT	Homo sapiens UDP-1-phucuronosyltransferase gene, complete cds		
11486 23835		8.73	8.0E-07 T07770.1	EST_HUMAN	EST05680 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBEN89		
11680 24108		7.98	8.0E-07 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C090		
1806 14461	27052	1.14	7.0E-07 AF167341.1	NT	Homo sapiens membrane Interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11		
5710 18330	30841	0.69	7.0E-07 60059700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA8), mRNA		
5710 18336	30842	0.69	7.0E-07 60059700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA8), mRNA		
10642 23174	36188	1.58	7.0E-07 BE070848.1	EST_HUMAN	7733g01_x1_NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298498 3' similar to TR-Q98897 Q86897 ENDOGENOUS RETROVIRUS-K, LTR U5 AND GAG GENE. :		
1856 14540	27098	2.58	6.0E-07 AW855558.1	EST_HUMAN	CN3-C170277-221088-024-611 CT0277 Homo sapiens cDNA		
2534 15098	27871	2.3	6.0E-07 AF010413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes; >		
4044 16842		1.78	8.0E-07 P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION		
8068 21005	34538	1.94	8.0E-07 BF001887.1	EST_HUMAN	7844f07_x1_NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3114149 3' similar to TR-O75820 O75820		
11025 24007	37131	1.83	6.0E-07 AJ702850.1	EST_HUMAN	cm87105_x5_NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:15541177 5'		
11049 24008		2.85	8.0E-07 AW803222.1	EST_HUMAN	CM4-NH1029-250320-121-h12 NH1029 Homo sapiens cDNA		
348 12398		1.19	5.0E-07 AI8311863.1	EST_HUMAN	wh84f10_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'		
1095 13700		2.21	5.0E-07 AA380630.1	EST_HUMAN	EST08615 Supr cells Homo sapiens cDNA 5' end		
3068 15381		0.84	5.0E-07 AI8311863.1	EST_HUMAN	wh84f10_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'		
4751 17332	26775	1.32	5.0E-07 AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds		
6268 18878	31644	1.13	5.0E-07 US65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds		
7124 19464	32281	1.56	5.0E-07 AI293881.1	EST_HUMAN	tg06805_x1_NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alt repetitive element; contains element A3R repetitive element ;		
7124 19464	32282	1.56	6.0E-07 AI293881.1	EST_HUMAN	tg06805_x1_NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alt repetitive element; contains element A3R repetitive element ;		
7386 18812	32778	16.07	5.0E-07 AW070885.1	EST_HUMAN	xo31ad2_x1_NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568342 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN)		
8217 20758	33872	0.82	5.0E-07 Q8WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)		

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8427	20867			1.06	5.0E-07 P09583	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10270	22795	35752	4.46	5.0E-07 A1B08587.1	EST_HUMAN	CM-BT178-220488-014 BT178 Homo sapiens cDNA LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
10542	23079	36093	1.59	5.0E-07 P08547	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR	
11391	23843	36907	4.94	5.0E-07 P11087	SWISSPROT		
11452	23902		2.43	5.0E-07 AJ271735.1	NT	Homo sapiens Xq pseudobautosomal region; segment 1/2	
123391	24889		2.85	5.0E-07 AW825337.1	EST_HUMAN	QY6-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA ws4Hn05_x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE-2504697 3'	
4071	16867	29129	1.84	4.0E-07 AW008602.1	EST_HUMAN	ws4Hn05_x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE-2504697 3'	
7230	19781		0.98	4.0E-07 AJ277285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	
7311	19839	32687	1.35	4.0E-07 Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE NHDA1)	
7311	19839	32688	1.35	4.0E-07 Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE NHDA1)	
7863	20405	33312	0.65	4.0E-07 AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007	
8981	21539	34445	5.37	4.0E-07 AW410134.1	EST_HUMAN	ny89p11_x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE-2856548 3'	
10228	22723	35715	0.5	4.0E-07 AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018	
10817	23338	36851	4.05	4.0E-07 A1785528.1	EST_HUMAN	W8TB08_x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE-2389703 3'	
10817	23338	36852	4.05	4.0E-07 A1785528.1	EST_HUMAN	W8TB08_x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE-2389703 3'	
11100	23610		2.08	4.0E-07 BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA	
468	13100	25581	4.51	3.0E-07 UJ18719.1	NT	Human microtubule-associated glycoprotein (MAP2) gene, putative promoter region and alternatively spliced untranslated exons	
609	13237	25711	2.84	3.0E-07 AJ271735.1	NT	Homo sapiens Xq pseudobautosomal region; segment 1/2	
1417	14010	26539	1.85	3.0E-07 M69149.1	NT	Human polymorphic microsatellite DNA	
1667	14200		1.95	3.0E-07 MB4857.1	NT	Human hK subgroup I gamma-like gene, exons 1 and 2, V-region 018 allele	
2060	14670		3.87	3.0E-07 AA526763.1	EST_HUMAN	ne66b09_s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE-890825 similar to contains Ali repetitive element; contains L1, L3, L1 repetitive element;	
2327	14898	27471	1.72	3.0E-07 M69149.1	NT	Human polymorphic microsatellite DNA	
2508	15072	27645	6.58	3.0E-07 BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA	
2508	15072	27648	6.58	3.0E-07 BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA	
3069	15684	28158	0.79	3.0E-07 TB4704.1	EST_HUMAN	yd50112_x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE-111665 5'	
3195	15807	28280	2.03	3.0E-07 P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	
4788	17388		0.58	3.0E-07 P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVONACROGLOBULIN)	
4834	17412	28885	7.74	3.0E-07 AY650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCQD01 3'	
4873	17453	28895	0.71	3.0E-07 A1787236.1	EST_HUMAN	we88612_x1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE-2347887 3'	
5222	17787	30265	1.81	3.0E-07 T57850.1	EST_HUMAN	yc14h00_s1 Stratogene lung (R837210) Homo sapiens cDNA clone IMAGE-80705 3' similar to similar to gb:AK23882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
52222	17787	30208	1.81	3.0E-07 T57850.1	EST_HUMAN	yc1410s.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:JAC62862 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)	
58471	18471	31197	12.79	3.0E-07 O88907	SWISSPROT	PROTEIN-ARGININE DEMINASE TYPE IV (PEPTIDYLARGININE DEMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEMINASE TYPE ALPHA)	
61228	18743	31498	0.71	3.0E-07 O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR	
68004	18395		5.41	3.0E-07 AA815175.1	EST_HUMAN	0046c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338690 3'	
75119	200339	32508	3.22	3.0E-07 AW7977168.1	EST_HUMAN	QV1-UML0036-280300-115-g02 UML0036 Homo sapiens cDNA clone QV1-UML0036-280300-115-g02 UML0036 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu	
76559	20171		1.6	3.0E-07 A1581065.1	EST_HUMAN	repetitive element;contains element MSR1 MSR1 repetitive element;	
11373	23825		1.68	3.0E-07 BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA	
12841	24716		6.74	3.0E-07 AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial	
31	12710	25168	3.38	2.0E-07 AF262888.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds	
165	12828	25314	7.81	2.0E-07 L77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric and	
165	12828	25315	7.81	2.0E-07 L77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric and	
194	12854	26338	45.63	2.0E-07 U38848.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds	
778	13397	25898	2.58	2.0E-07 AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	
778	13397	25899	2.58	2.0E-07 AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	
781	13409		0.91	2.0E-07 P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	
979	13581	28106	2.56	2.0E-07 AA223260.1	EST_HUMAN	2708807.s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:8508869 3' similar to gb:1-31880 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element	
980	13582	28107	6.68	2.0E-07 T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;	
1205	13605	28318	0.76	2.0E-07 Q28798	SWISSPROT	V6 AUTOANTIGEN	
1644	14238	28771	1.88	2.0E-07 Q09701	SWISSPROT	HYPOTHETICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1	
3879	16280		0.65	2.0E-07 BF131397.1	EST_HUMAN	601818916F1 NIH_M3C_58 Homo sapiens cDNA clone IMAGE:4044891 5'	
3751	16552	28820	22.38	2.0E-07 AF125348.1	NT	Homo sapiens cavin1 (CAV1) gene, exon 3 and partial cds	
5547	18179	30593	1.81	2.0E-07 AW888038.1	EST_HUMAN	RC3-NIN0068-280400-021-g11 NIN0068 Homo sapiens cDNA	
6769	18682	32171	1.59	2.0E-07 AI208715.1	EST_HUMAN	0958d05.x1 Scores_Bests_NHT Homo sapiens cDNA clone IMAGE:1839177 3'	
8405	20945		3.57	2.0E-07 AV728390.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'	
8628	21167	34082	1.1	2.0E-07 AA035198.1	EST_HUMAN	2k27g06.s1 Scores_Pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:477808 3'	
8678	22175		2.27	2.0E-07 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
10168	22063	35658	5.85	2.0E-07 AW882507.1	EST_HUMAN	CM4-NIN003-280300-124-e06 NIN0003 Homo sapiens cDNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10383	22877	35888	0.76	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10383	22877	35889	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11842	24683			2.67	2.0E-07	BE153171.1	EST_HUMAN
11734	24890			3.56	2.0E-07	AI732462.1	EST_HUMAN
1141	13744			1.17	1.0E-07	AL163282.2	NT
2013	14595	27157	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C0313
2013	14595	27158	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C0313
2424	14982	27585	0.83	1.0E-07	P10283	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2854	14162	26893	2.94	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3807	13744			1.22	1.0E-07	AL163282.2	NT
4380	16987	29413	2.75	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNFO4 5'
4380	16987	29414	2.76	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNFO4 5'
6827	19223	32028	1.57	1.0E-07	U92671.2	NT	Homo sapiens chromosome 21 segment HS21C0322
6860	19527	32249	4.57	1.0E-07	BE047871.1	EST_HUMAN	BE047871.1 NCI OGAP_Bm52 Homo sapiens cDNA clone IMAGE:22811339 5'
6860	19527	32250	4.57	1.0E-07	BE047871.1	EST_HUMAN	BE047871.1 NCI OGAP_Bm52 Homo sapiens cDNA clone IMAGE:22811339 5'
7504	20028	32890	8.62	1.0E-07	IN55081.1	EST_HUMAN	IN55081.1 Scareas fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7844	20198	33042	0.82	1.0E-07	BF375809.1	EST_HUMAN	BF375809.1 NCI OGAP_Bm52 Homo sapiens cDNA clone IMAGE:22811339 5'
7844	20198	33043	0.82	1.0E-07	BF375809.1	EST_HUMAN	BF375809.1 NCI OGAP_Bm52 Homo sapiens cDNA clone IMAGE:22811339 5'
7889	20181	33088	1.35	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C0381
8157	20688	33611	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8157	20688	33612	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8884	21422	34347	2.7	1.0E-07	AA3863578.1	EST_HUMAN	Z51610.s1 Scareas fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:434346 3'
9194	21711	34654	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS & PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9535	22035	34995	0.49	1.0E-07	BE327843.1	EST_HUMAN	hu28n08.s1 NCI CGAP_Mat15 Homo sapiens cDNA clone IMAGE:31714119 3' similar to contains MER18.13
9849	22347	35329	2.51	1.0E-07	BF874524.1	EST_HUMAN	MER18 repetitive element: 802137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
9855	22353	35334	1.19	1.0E-07	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
10362	22856		3.53	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C0382

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Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12013	24860	30704	2.42	1.0E-07	BE048770.1	EST_HUMAN	hr53ct11_x1 NCI_CGAP_Kir11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:085722_085722
7325	19852	32714	0.87	8.0E-08	AI539342.1	EST_HUMAN	l651908_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:20001195 3'
8802	22390	35285	2.1	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cDNA clone cdABFB08 5'
11081	23573	36810	3.41	9.0E-08	AI891052.1	EST_HUMAN	wn36a7_x1 NCI_CGAP_Gs4 Homo sapiens cDNA clone IMAGE:2446362 3' similar to contains OFR_12
11510	23987	37039	4.51	9.0E-08	AI163301.2	NT	ORF repetitive element;
11981	24283		2.88	9.0E-08	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C101
635	15420		2.27	8.0E-08	AI911352.1	EST_HUMAN	wd18a05_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23262273 3'
1088	13683		0.78	8.0E-08	BE785469.1	EST_HUMAN	6011590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843978 5'
3598	16202		1.05	8.0E-08	BE785469.1	EST_HUMAN	6011590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843978 5'
8874	21213	34133	3.54	8.0E-08	AI732387.1	EST_HUMAN	cn15c02_x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8874	21213	34134	3.54	8.0E-08	AI732387.1	EST_HUMAN	cn15c02_x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9545	22045	35008	3.32	8.0E-08	AW970683.1	EST_HUMAN	EST3&2778 MAGE resequences, MAGK Homo sapiens cDNA
11124	23632		2.61	8.0E-08	AF253417.1	NT	Homo sapiens microsatellite hydrolase (EPHX1) gene, complete cds
84	12760	25243	2.82	7.0E-08	QR22367	SWISSPROT	ANKYRIN (ERYTHROCYTE ANKYRIN)
1405	13698	26827	11.98	7.0E-08	XO4898.1	NT	Ref mRNA for ribosomal protein L31
3835	16238	28113	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYNC)
3635	16238	28114	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYNC)
4002	16800	28073	0.89	7.0E-08	P01806	SWISSPROT	IG KAPPA CHAIN VI REGION QU
4002	16800	28074	0.89	7.0E-08	P01806	SWISSPROT	IG KAPPA CHAIN VI REGION QU
10683	23223		8.5	7.0E-08	AI535743.1	EST_HUMAN	cang3_F11A5 canon Homo sapiens cDNA 3'
11523	23871	37041	6.1	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12450	16238	28713	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYNC)
12450	16238	28714	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYNC)
850	13488	25974	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
850	13488	25975	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2401	14969	27543	2.01	6.0E-08	BE14398.1	EST_HUMAN	MFR0-HT0168-1911188-004-009 HT0168 Homo sapiens cDNA
4334	16921	28363	1.14	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7892	20434		0.68	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9251	21777		0.6	6.0E-08	AA827075.1	EST_HUMAN	cb56c5.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335388 3' similar to contains MER12_b3 MER12 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor [CONTAINS: REVERSE TRANSCRIPTASE ; RETROVIRUS-RELATED POLYPROTEIN ; ENDONUCLEASE]
11283	23745	38802	2.61	6.0E-08	P11369	SWISSPROT	
11407	23858		1.77	6.0E-08	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C009
88	12784	25247	2.33	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2277	14851	27429	1.23	5.0E-08	AA483851.1	EST_HUMAN	rh03508_s1 NC1 CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alt repetitive element.
11682	24107		7.32	5.0E-08	P06981	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11889	24233	31004	1.48	5.0E-08	AW851878.1	EST_HUMAN	Q00-C10225-131088-034-012 CT0225 Homo sapiens cDNA
1787	14387	28861	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1787	14387	28862	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2810	15527		1.49	4.0E-08	AL079581.1	EST_HUMAN	DKF434-0428_11_484 (synonym: hits3) Homo sapiens cDNA clone DKF74-0428 5'
3100	15715		1.01	4.0E-08	A1078417.1	EST_HUMAN	cd015a02_x1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alt repetitive element.
38986	16584	28055	0.87	4.0E-08	U826988.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6537	19138	31928	1.14	4.0E-08	P52824	SWISSPROT	URIDINE PHOSPHORYLASE (URIDYLATE)
8733	21272	34192	0.57	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
90889	21603	34533	0.92	4.0E-08	L42571.1	NT	Chitobiosidase ribosomal transcription factor (UBF2) mRNA, complete cds
95683	22063		0.87	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10233	22723		0.71	4.0E-08	A1016342.1	EST_HUMAN	ct78d12_s1 Soares_fetal_tissue_Nb2HFB_9W Homo sapiens cDNA clone IMAGE:1622903 3'
10287	22782	35774	3.59	4.0E-08	A1050027.1	EST_HUMAN	ct22d10_x1 Gesseler_Wilms tumor_Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alt repetitive element/contains element MER22 repetitive element;
10732	23308		1.7	4.0E-08	AJ258817.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
10989	23483	38510	3.7	4.0E-08	BF892483.1	EST_HUMAN	60224824F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
10988	23483	38511	3.7	4.0E-08	BF892483.1	EST_HUMAN	60224824F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11697	25022		1.4	4.0E-08	W76159.1	EST_HUMAN	2885903_s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1_H1 repetitive element;
12378	24546		3.48	4.0E-08	A1343353.1	EST_HUMAN	L1_H1 repetitive element; MER18 MER18 repetitive element;
5785	18420	31138	3.12	3.0E-08	BE018348.1	EST_HUMAN	bb78a10_y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR-Q92158 Q9Z158
7052	18071	30462	3.77	3.0E-08	A1792737.1	EST_HUMAN	SYNTAXIN 17;
7545	20005	32839	1.41	3.0E-08	AL163246.2	NT	q870f11_s1 NC1 CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1844045 5'
							Homo sapiens chromosome 21 segment HS21C008

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7730 20238				4.17 3.0E-08	AI483352.1 AF055086.1	EST_HUMAN NT	hs3hb9_x1_Scores_NSF_F8_8W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSSABLE ELEMENT; COMPLETE CONSENSUS SEQUENCE.;
8812 22210				0.51 3.0E-08			Homo sapiens MHC class 1 region
11682 24087				38.65 3.0E-08	R18420.1 AW302886.1	EST_HUMAN EST_HUMAN	Y0234_x1_Scores_Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains AU repetitive element;
220 12881				6.74 2.0E-08			xr8706_x1_NCI_CGAP_L028 Homo sapiens cDNA clone IMAGE:2787139 3'
247 12907				0.48 2.0E-08	AA425688.1 AF183349.1	EST_HUMAN EST_HUMAN	zw4807_x1_Scores_biot_fetus_NB2hf38_3w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains ATU repetitive element;contains element MER15 repetitive element;
622 13164	25637			2.59 2.0E-08		NT	Guttag galus Dach2 protein (Dach2) mRNA, complete cds
688 13312	25798			10.98 2.0E-08	AW884438.1 AW884438.1	EST_HUMAN EST_HUMAN	MRO-C10080-240200-001-98 O70080 Homo sapiens cDNA
688 13312	25797			10.98 2.0E-08	AW884438.1 BE280477.1	EST_HUMAN EST_HUMAN	MRO-C10080-240200-001-98 O70080 Homo sapiens cDNA clone IMAGE:3138863 5'
1027 13638				22.68 2.0E-08		NT	Homo sapiens chromosome 21 segment HS21C047
1387 13861	26508			2.08 2.0E-08	AL183247.2 BE734871.1	EST_HUMAN EST_HUMAN	601570_4633F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845188 5'
1777 14367				1.3 2.0E-08			
1895 14480				4.65 2.0E-08	AW270271.1 AW270271.1	EST_HUMAN EST_HUMAN	404311_x1_NCI_CGAP_HN1 Homo sapiens cDNA clone IMAGE:2743149 3'
2462 15029	27597			0.97 2.0E-08	AA731948.1 K00216.1	EST_HUMAN NT	mm3401_s1_NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L163 L1 repetitive element;
2580 15143				2.21 2.0E-08			Sheep Hs-rRNA-GUG
3243 15885	28337			6.85 2.0E-08	O42280 O42280	SWISSPROT SWISSPROT	WNT-14 PROTEIN PRECURSOR WNT-14 PROTEIN PRECURSOR
3243 15885	28338			6.85 2.0E-08			
3928 16524				1.83 2.0E-08	AW913620.1 U82868.1	EST_HUMAN EST_HUMAN	RC3-ST0197-7-61086-012-b03 ST0197 Homo sapiens cDNA Homo sapiens shag gene, alternatively spliced products, complete cds
4152 18744	28198			0.57 2.0E-08			uc28d57_x1_NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:314360 5' similar to contains L172 L1 repetitive element;
4464 17079				1.74 2.0E-08	AA456040.1 AA813204.1	EST_HUMAN EST_HUMAN	hs17hd8x2_x1_NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:20109327 3' similar to contains MER18 b3 repetitive element;
5082 17985				3.83 2.0E-08	AW572881.1 AA813204.1	EST_HUMAN EST_HUMAN	ai80h11_s1_Scores_Itesta_NHT_Homo sapiens cDNA clone 1377189 3'
5917 18441	31163			0.87 2.0E-08			xd32c04_x1_NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2582462 3' similar to contains MER18 b3
5998 18618	31954			0.87 2.0E-08	AW0888924.1 P10272	EST_HUMAN SWISSPROT	MER18 MER18 repetitive element; POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
7946 20488	33389			1.07 2.0E-08			
8054 20596	33503			1.12 2.0E-08	AA490121.1 AU139878.1	EST_HUMAN EST_HUMAN	ab02g831 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:3386743 AU139878 PLACE Homo sapiens cDNA clone PLACE:1011710 5'
8014 21551				1.41 2.0E-08			

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Meet Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413 22807	35904	0.78	2.0E-08	N78097.1	EST_HUMAN	W7202.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:248283 5' similar to contig LTR1.6S LTR1 repetitive element;	
10413 22807	35905	0.78	2.0E-08	N78097.1	EST_HUMAN	W7202.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:248283 5' similar to contig LTR1.6S LTR1 repetitive element;	
11882 24283		1.74	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
12659 25073		1.44	2.0E-08	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds	
18112 14402	26847	0.89	1.0E-08	AF125348.1	NT	Homo sapiens cavinin 1 (CAV1) gene, exon 3 and partial cds	
20905 14674		2.74	1.0E-08	BE141858.1	EST_HUMAN	PM2-HT10130-150808-001-f12 HTD10130 Homo sapiens cDNA	
57865 18410	311128	4.23	1.0E-08	AJ010770.1	NT	Homo sapiens hyaluronan gene, exons 1-50	
7746 20254	33148	1.14	1.0E-08	P19474	SWISSPROT	62 KD RIO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) / (RQ(SS-A))	
7978 20520	33428	0.55	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102	
8070 20612	33526	0.85	1.0E-08	AF224689.1	NT	Homo sapiens mannose-6-phosphate, beta 1,4-lycosidase (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	
8070 20612	33528	0.85	1.0E-08	AF224689.1	NT	Homo sapiens mannose-6-phosphate, beta 1,4-lycosidase (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	
8484 21023	33840	1.84	1.0E-08	AI015304.1	EST_HUMAN	035605.1 Scores cDNA clone IMAGE:1618738 3'	
9132 21087	34808	0.75	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA	
8870 22373	35350	1.16	1.0E-08	P78110	SWISSPROT	TRICARBOXYLATE CARRIER PROTEIN (CITRATE TRANSPORT PROTEIN) (CTP)	
10449 22843	35853	0.64	1.0E-08	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	
11185 23700	36751	3.79	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class II region	
12081 24353		2.27	1.0E-08	X51755.1	NT	Human lamda-dannoglobulin constant region complex (gamma-like)	
4327 16913	26858	3.93	8.0E-08	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
4327 16913	26957	3.93	8.0E-08	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	
8874 22469		0.49	9.0E-09	197850.1	EST_HUMAN	yester12.61 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121918 3'	
7308 19850	32284	8.03	8.0E-09	AI163500.1	EST_HUMAN	qd4280/7.21 Scores fetal liver_ NbHH16W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.1 MSR1 repetitive element;	
7942 20484	33398	2.98	8.0E-09	AW900169.1	EST_HUMAN	CAG-NN1004-100500-273-008 NN1004 Homo sapiens cDNA	
8919 21457		2.77	8.0E-09	AA838682.1	EST_HUMAN	cp74d8.51 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'	
3687 16288		1.87	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketothio-CoA thiolase beta-subunit of mitochondrial trifunctional protein. seqn 2-3	
4050 16670		1	7.0E-09	U56871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7843	20385		0.5	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29_b2 MER29 repetitive element;
7901	20533		0.78	7.0E-09	AA2556200.1	EST_HUMAN	zr80c58.r1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:381882 5' similar to contains L1.12 L1 repetitive element;
9184	21701	34844	2.98	7.0E-09	LD9709.1	NT	Human lysosomal membrane glycoprotein 2 (LAMP2) gene, 5' end and flanking region
10088	22581	35574	1.3	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10248	22743		0.63	7.0E-09	AA058526.1	EST_HUMAN	zf58e07..61 Soares retina N284IR Homo sapiens cDNA clone IMAGE:3811158 3' similar to contains L1.12 L1 repetitive element;
10552	23088		2.78	7.0E-09	T97850.1	EST_HUMAN	y658a12..61 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2198	14774		1.16	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514..71_434 (synonym: hbsc2) Homo sapiens cDNA clone DKFZp434C0514 5'
5118	17688	30128	5.44	6.0E-09	BE169421.1	EST_HUMAN	PM1+TT0527..180200-001-h05 HT0527 Homo sapiens cDNA
5246	17810	30232	1	6.0E-09	AW593471.1	EST_HUMAN	hg16f12..x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2845807 3' similar to gb:X53743 FIBULIN-1 ISOFORM C PRECURSOR (HUMAN);
6248	17810	30233	1	6.0E-09	AW593471.1	EST_HUMAN	hg16f12..x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2845807 3' similar to gb:X53743 FIBULIN-1 ISOFORM C PRECURSOR (HUMAN);
5582	18213	30982	12.11	6.0E-09	AW185784.1	EST_HUMAN	xn85h08..x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8512	21051	33973	0.81	6.0E-09	BE161653.1	EST_HUMAN	MR3+TT0448-260300-201-h12 HT0448 Homo sapiens cDNA
9103	21639	34578	2.37	6.0E-09	4503710 NT		Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10177	22672		3.89	6.0E-09	AF2008923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10610	23143	36154	1.68	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29_b2 MER29 repetitive element;
1460	14052	26584	3.95	5.0E-09	BE148284.1	EST_HUMAN	RC2+TT0522-120200-014-h10 HT0522 Homo sapiens cDNA
1883	14478	27038	0.83	5.0E-09	AL1083284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6542	19141	31833	2.28	5.0E-09	AA358454.1	EST_HUMAN	EST88748 Fetal lung II Homo sapiens cDNA 5' end
8521	21060	338983	0.59	5.0E-09	P37071	SWISSPROT	Olfactory receptor-like protein COR5
10007	22502	35493	2.27	5.0E-09	AW798987.1	EST_HUMAN	PM2+UM0053-240300-008-c08 UM0053 Homo sapiens cDNA
547	13178		1.69	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1000	13611		1.88	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1518	14110	28848	1.81	4.0E-09	85589718 NT		Homo sapiens hypothetical protein (AFU38168), mRNA
2473	15040	27608	4.54	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to heat shock protein, 80 kDa
7788	20331	33237	0.72	4.0E-09	AA495747.1	EST_HUMAN	zv04c58..r1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:768288 5'
8458	20869	33915	0.62	4.0E-09	T8942.1	EST_HUMAN	yd11507..51 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:868804 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10898	23510			1.73	4.0E-09 AA105142.1	EST_HUMAN	234e12_r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:385278 5' similar to gb:L07807
2390	14958	27530		6.83	3.0E-09 BE222239.1	EST_HUMAN	DYNA1N1 (HUMAN); In08689_r1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180120 3' similar to contains MER18_13 MER18 repetitive element;
2589	15151	27717		0.95	3.0E-09 BE222239.1	EST_HUMAN	In08689_r1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180120 3' similar to contains MER18_13 MER18 repetitive element;
2877	15235	27802		1.22	3.0E-09 P23249	SWISSPROT	PROTEIN MOV-10
3372	15980	28457		1.05	3.0E-09 BE222239.1	EST_HUMAN	In08689_r1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180120 3' similar to contains MER18_13 MER18 repetitive element;
3423	16031			3.13	3.0E-09 AA442272.1	EST_HUMAN	Zf5464_r1 Soares_NHT_Homo sapiens cDNA clone IMAGE:757422 5'
4172	16763			3.64	3.0E-09 X16874.1	NT	H_sapiens PADPRP-1 gene for NAD(+)-ADP-ribosyltransferase
4517	17101	29549		5.18	3.0E-09 AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4610	17183	28639		1.52	3.0E-09 Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
7841	20383	33287		1.29	3.0E-09 BE485780.1	EST_HUMAN	In0804022_r1 NCI_CGAP_KH11 Homo sapiens cDNA clone IMAGE:31804080 3' similar to TR-O55091
10148	22641	35631		1.98	3.0E-09 AL168247.2	NT	Home sapiens chromosome 21 segment HS21CQ47
10800	22420	36437		3.87	3.0E-09 BF106843.1	EST_HUMAN	7172c08_r1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:352707030 3'
10800	22420	36438		3.87	3.0E-09 BF106843.1	EST_HUMAN	7172c08_r1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:352707030 3'
845	13461			1.01	2.0E-09 X16874.1	NT	H_sapiens PADPRP-1 gene for NAD(+)-ADP-ribosyltransferase
1301	13886	28417		6.02	2.0E-09 AL168284.2	NT	Home sapiens chromosome 21 segment HS21CQ84
1688	14281			10.31	2.0E-09 AL118573.1	EST_HUMAN	DKFZp761B1710_r1 781 (synonym: hany2) Homo sapiens cDNA clone DKFZp761B1710_5'
2364	14835	27507		2.78	2.0E-09 Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
4011	18609	28082		4.13	2.0E-09 Q6D041	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4083	18678	28139		0.94	2.0E-09 AL263478.1	EST_HUMAN	qf07d89_r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
6876	18610			0.74	2.0E-09 AA357407.1	EST_HUMAN	EST88142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7474	18998	32881		8.48	2.0E-09 AA481430.1	EST_HUMAN	zg63H06_r1 Soares_total_fetus_NB2HIF8_9W Homo sapiens cDNA clone IMAGE:7981187 5' similar to contains Alu repetitive element
7532	20052	32925		0.68	2.0E-09 W26834.1	EST_HUMAN	62d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8848	21185	34104		1.72	2.0E-09 AF271735.1	NT	Home sapiens Xq pseudautosomal region: segment 1/2
11634	24074			1.72	2.0E-09 AF111168.2	NT	Home sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12238	13461			27.08	2.0E-09 X16874.1	NT	H_sapiens PADPRP-1 gene for NAD(+)-ADP-ribosyltransferase
12310	25094			2.25	2.0E-09 AA226070.1	EST_HUMAN	nc11022_r1 NCI_CGAP_Pri Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element

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Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1032	13842			1.14	1.0E-09 W78152.1	EST_HUMAN	zr79d03_s1 Scores: fetal_heart NIH-H18W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:LR2832 PROXISOME ACTIVATED RECEPTOR ALPHA (HUMAN);
1148	13751	26280	2.3	1.0E-09	5031624_NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	
1148	13751	26281	2.3	1.0E-09	5031624_NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	
2814	15531	26003	1.74	1.0E-09 U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b472p44) gene, partial cds, neuronal apoptosis inhibitory protein (napip) and survival motor neuron protein (smn) genes, complete cds	
2662	15568	26042	3.98	1.0E-09 M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NP41) mRNA, complete cds	
2662	15568	26043	3.98	1.0E-09 M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NP41) mRNA, complete cds	
3073	15688	26160	0.77	1.0E-09 BE535440.1	EST_HUMAN	601058802F1 NIH MGIC 10 Homo sapiens cDNA clone IMAGE:3446777 5'	
4916	17491			5.48	1.0E-09 AA719287.1	EST_HUMAN	zr35b03_s1 Scores: phaseI island N3HPG Homo sapiens cDNA clone IMAGE:4140289 3' similar to contains Alu repetitive element-contains element MER22 repetitive element;
5694	18320	30819	0.87	1.0E-09 AL1692283.2	NT	Homo sapiens chromosome 21 segment HS21C083	
5696	18816	31352	1.46	1.0E-09 U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
6263	18901	31871	3.17	1.0E-09 P26894	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	
8320	20870	33784	0.87	1.0E-09 AL689474.1	EST_HUMAN	wd39b06_x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.1 MER25 repetitive element;	
10216	22711		2.57	1.0E-09 AL1692283.2	NT	Homo sapiens chromosome 21 segment HS21C083	
12138	25032	30820	3.3	1.0E-09 11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	
12563	24944		1.82	1.0E-09 AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	
1352	13947	28471	1.48	9.0E-10 AW867740.1	EST_HUMAN	MRO-SN040-050500-002-c07 SN0040 Homo sapiens cDNA	
2860	15479	27955	6.87	9.0E-10 AI870071.1	EST_HUMAN	wr78b03_x1 Scores: Deckenfests_codon_NHCD Homo sapiens cDNA clone IMAGE:2247253 3' similar to SW:RL29 HUMAN_Pt7814 60S_RIBOSOMAL PROTEIN L29 ;contains element PR5 repetitive element;	
6922	19581	32410	4.35	9.0E-10 AI452982.1	EST_HUMAN	y44b0372_C00372 PUTATIVE_P150_;	
158	12821	25309	10.47	8.0E-10 U63630_2	NT	Homo sapiens NSF_F8_gW_OT PA_P_S1 Homo sapiens cDNA clone QV1-B1_0631-150200-071-01 BT0631 Homo sapiens cDNA	
3368	15995	28472	0.59	8.0E-10 BE5080748.1	EST_HUMAN	EST85684 Small intestine I Homo sapiens cDNA 5' end	
4279	16895	29311	4.11	8.0E-10 AA376832.1	EST_HUMAN	Home sapiens lens major intrinsic protein (MIP) gene, complete cds	
9875	22372		2.34	8.0E-10 U38308_2	NT	Home sapiens TPA inducible protein (LOC51588), mRNA	
730	13350	25844	24.84	7.0E-10 7706225	NT	Home sapiens TPA inducible protein (LOC51588), mRNA	
1863	14256	28791	2.13	7.0E-10 Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)	
2067	14847		1.31	7.0E-10 P08548	SWISSPROT	UNE-1 REVERSE TRANSCRIPTASE HOMOLOG	
2594	15158		13	7.0E-10 P08547	SWISSPROT	UNE-1 REVERSE TRANSCRIPTASE HOMOLOG	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3124	15738	28206	2.84	7.0E-10	X008868.1	NT	Homo sapiens DHFR gene, exon 3
6332	18838	31714	5.26	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Cell bladder II Homo sapiens cDNA 5' end
7446	18970	32838	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-1110700-209-D12 HT0619 Homo sapiens cDNA
7852	23184		1.43	7.0E-10	P25884	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II/LARGE SUBUNIT
7816	23458	33384	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
7916	23458	33385	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10212	22707	35701	0.57	7.0E-10	L08885.1	NT	Homo sapiens MADSMEF2-family transcription factor (MEF2C) mRNA, complete cds
11511	23659	37030	1.54	7.0E-10	AW778789.1	EST_HUMAN	hod2q20.21 NCI_CGAP_Cof4 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Atu repetitive element; contains MER7 b1 MER7 repetitive element;
948	13559	26072	3.68	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2702	15359	27827	1.89	6.0E-10	AI24405.1	EST_HUMAN	102607_x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2085021 3'
4847	17225		2.16	6.0E-10	AW853718.1	EST_HUMAN	RC3-C170254-031089-012-g12 CT0254 Homo sapiens cDNA
8718	21297	34177	0.94	6.0E-10	P33790	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8718	21297	34178	0.94	6.0E-10	P33790	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
8552	22052	35015	0.52	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
11731	24136		1.47	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
792	12140		6.2	6.0E-10	AL049804.1	EST_HUMAN	EST384012 MAGE sequences, MAGL Homo sapiens cDNA
3522	16127	28807	0.98	5.0E-10	Q01033	SWISSPROT	DKFZp434N219_f1_434 (synonym: Ites3) Homo sapiens cDNA clone DKFZp434N219_5'
5002	17575	30018	1.05	5.0E-10	AW028877.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
5002	17575	30019	1.05	5.0E-10	AW028877.1	EST_HUMAN	w97b03_x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2542081 3' similar to contains MER10.H1 MER10 repetitive element;
5128	17700	30134	1.37	5.0E-10	AF181897.1	NT	w97b03_x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2542081 3' similar to contains MER10.H1 MER10 repetitive element;
7363	18868		1.84	5.0E-10	BF165159.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
8455	21881	34832	1.65	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
8455	21881	34833	1.65	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK888.8 IN CHROMOSOME III
						SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK888.8 IN CHROMOSOME III
118	12187		1.02	4.0E-10	AI221083.1	EST_HUMAN	pp03809.1 Scores_placenta_Beta2microglobulin_2NtBiproteinW Homo sapiens cDNA clone IMAGE:1758049 3'
607	13235	26709	0.73	4.0E-10	AA515280.1	EST_HUMAN	similar to contains LTR8_b2LTR8 repetitive element;
2039	14821	27189	1.17	4.0E-10	AW534708.1	EST_HUMAN	PP4401.61 NCI_CGAP_G63 Homo sapiens cDNA clone IMAGE:324848 3'
						NT	hg58g03_x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946844 3' similar to contains Atu repetitive element;

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2609 15171	27739		4.19	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7228 19759	32614		22.35	4.0E-10	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10097 22582	35584		0.62	4.0E-10	AW28243.1	EST HUMAN	U1-H-B12-ant-07-0-U.1.s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2727001 3'
10342 22838	35831		1.01	4.0E-10	AI287342.1	EST HUMAN	apf83h11.x1 Stanley Frontal SN pod 2 Homo sapiens cDNA clone IMAGE:2035853
948 13580	26074		1.85	3.0E-10	N36113.1	EST HUMAN	Y42708.s1 Soenes melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272803 3' similar to contains L1 H1 L1 repetitive element.
13985 13989			4.43	3.0E-10	AY065180.1	NT	Homo sapiens extracellular glycoprotein lectin precursor, gene, complete cds
46833 17218	28867		1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
46833 17218	28868		1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5846 18274	30748		0.92	3.0E-10	N50109.1	EST HUMAN	Y21190.s1 Soenes multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6350 18865	31134		1.87	3.0E-10	P20350	SWISSPROT	RHOMBOID PROTEIN (VENET PROTEIN)
6492 18053	31877		2.86	3.0E-10	BE302970.1	EST HUMAN	baf760B.1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
7737 20245	33138		2.3	3.0E-10	AV743302.1	EST HUMAN	AV743302 CB Homo sapiens cDNA clone CEBFGD008 5'
7737 20245	33137		2.3	3.0E-10	AV743302.1	EST HUMAN	AV743302 CB Homo sapiens cDNA clone CEBFGD008 5'
88865 21204	34122		1.08	3.0E-10	H87208.1	EST HUMAN	Y574b12.s1 Soenes ratia N2b-4f1R Homo sapiens cDNA clone IMAGE:205111 3' similar to contains MER28 repetitive element.
8978 21517	34442		1.81	3.0E-10	AW850731.1	EST HUMAN	IL3-CT0219-160200-084-B08 CT0219 Homo sapiens cDNA
8978 21517	34443		1.61	3.0E-10	AW850731.1	EST HUMAN	IL3-CT0219-160200-084-B08 CT0219 Homo sapiens cDNA
9284 21790			0.86	3.0E-10	AF026503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT7) gene, exon 5
10359 22833			2.13	3.0E-10	T65989.1	EST HUMAN	yc11e12.1 Stratagene lung (#837710) Homo sapiens cDNA clone IMAGE:303598 5'
10485 22978			1.71	3.0E-10	AA768284.1	EST HUMAN	nz28g03.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12415 24598	30011		3.44	3.0E-10	BE179817.1	EST HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
38 12717	25178		92.78	2.0E-10	P468988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38 12717	25177		92.78	2.0E-10	P468988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1942 14528			2.33	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (tf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3015 15581			0.66	2.0E-10	BF679447.1	EST HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:427337 6'
5971 18582			7.24	2.0E-10	Q28840	SWISSPROT	(HPRG)
6398 18001	31778		1.42	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7414 18639	32803		7.79	2.0E-10	BE781082.1	EST HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7856	20498	33407	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
7856	20498	33408	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
					7078d08.x1 NCI_CGAP_Kd1 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1 repetitive element ;		
9226	21742		0.85	2.0E-10	BF434595.1	EST_HUMAN	
1556	14748		2.26	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN00338-280300-001-f01 SN00338 Homo sapiens cDNA
1650	14242	26776	2.41	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC_Homo sapiens cDNA clone GL_CCGXA11 3'
2618	15180		1.78	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3548	18152	29834	0.73	1.0E-10	AW852812.1	EST_HUMAN	QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA
3583	16187		0.62	1.0E-10	AL041685.1	EST_HUMAN	DKFZp454N1317_11_434 (synonym: hits:3) Homo sapiens cDNA clone DKFZp454N1317 5'
3911	16197		0.89	1.0E-10	AL041685.1	EST_HUMAN	DKFZp454N1317_11_434 (synonym: hits:3) Homo sapiens cDNA clone DKFZp454N1317 5'
4087	16883		6.83	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4207	16798	29243	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4207	16798	29244	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4214	16803	29253	1.95	1.0E-10	AB091089.1	NT	Homo sapiens PCCX1 mRNA for protein containing COXC domain 1, complete cds
4249	16837		2.53	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5343	17804		1	1.0E-10	AJ787745.1	EST_HUMAN	WP-B2104.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MERS3;H MER31 repetitive element ;
8182	20723	33637	1.08	1.0E-10	AW408890.1	EST_HUMAN	FB_8A4_Fetal brain library Homo sapiens cDNA
					Q040410.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element ;		
8589	21128		1.03	1.0E-10	AJ288240.1	EST_HUMAN	
10103	22598		4.16	1.0E-10	AA001888.1	EST_HUMAN	2723-568.11 Strategene neuroepithelium NT2RAMI 8317234 Homo sapiens cDNA clone IMAGE:548814 5'
10783	23316	36325	3.47	1.0E-10	AJ036280.1	EST_HUMAN	QY65H03.x1 Scores_fetal_liver_spleen cDNA clone IMAGE:1672881 3'
11672	18038		1.58	1.0E-10	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IFPP2, TAP1, LMP7, TAP2, DOB3, DQB2 and RING38, 9, 13 and 14 genes
283	12839	25425	0.88	9.0E-11	BE145800.1	EST_HUMAN	IL2-HT0203-291089-016-e08 HT0203 Homo sapiens cDNA
2152	14729	27302	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp454T0225_11_547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp454T0225 5'
2152	14729	27303	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp454T0225_11_547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp454T0225 5'
3430	18038	28520	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp454T0225_11_547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp454T0225 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	16038	28521	2.33	9.0E-11 AL134395.1	EST HUMAN	DKFZp547D225	l 547 (synonym: Ifibr1) Homo sapiens cDNA clone IMAGE:970225 5'
4568	17182	28620	0.89	9.0E-11 AA775985.1	EST HUMAN	aa7801..s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'	
5763	18389		3.77	9.0E-11 BE079780.1	EST HUMAN	RC-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA	
10058	22553	35548	0.86	9.0E-11 AA324980.1	EST HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end	
10058	22553	35549	0.86	9.0E-11 AA324980.1	EST HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end	
12050	24342	30889	3.62	9.0E-11 C16835.1	EST HUMAN	C16835 Okinawa human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506898 5'	
3150	15784		0.98	8.0E-11 YH531f11.s1 Soares adult brain N265HIB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;			
4035	18833	26102	0.68	8.0E-11 AJ478817.1	EST HUMAN	mm54089..x1 NCI CGAP_KM11 Homo sapiens cDNA clone IMAGE:2101800 3'	
4117	18711	28165	5.2	8.0E-11 N23712.1	EST HUMAN	yyr6006..s1 Weizmann Olfactory Epithelium I Homo sapiens cDNA clone IMAGE:265288 3'	
1487	14089	28629	2.94	7.0E-11 AA330842.1	EST HUMAN	EST34392 Embryo, 8 week I Homo sapiens cDNA 5' end	
39389	16537	28004	0.84	7.0E-11 AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor	
8435	20975	33989	2.61	7.0E-11 AF186884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	
10128	22624		1.1	7.0E-11 P11368	SWISSPROT	RETRORVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	
12206	24430		1.52	7.0E-11 AV701656.1	EST HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'	
437	13070	25568	6.57	6.0E-11 M65270.1	NT	Human matrix Gla Protein (MGP) gene, complete cds	
437	13070	25567	6.57	6.0E-11 M65270.1	NT	Human matrix Gla Protein (MGP) gene, complete cds	
6822	19412	32229	1.03	6.0E-11 L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6 phosphate dehydrogenase (GAPD) gene, complete cds's	
7680	20191	33080	3.20	6.0E-11 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
8205	20846	33768	3.25	6.0E-11 AV727859.1	EST HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCAS08 5'	
12	12881	25147	0.9	5.0E-11 AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083	
3411	12881	25147	1.29	5.0E-11 AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083	
4212	16898	28343	1.04	5.0E-11 P48034	SWISSPROT	ALDEHYDE OXIDASE	
68338	18235	32037	3.02	5.0E-11 AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013	
7537	20057	32831	12.3	5.0E-11 11416794	NT	Homo sapiens protocadherin beta 3 (PCDH18B), mRNA	
1446	14038		1.41	4.0E-11 AA436042.1	EST HUMAN	201612..1 Soares testis NT11 Homo sapiens cDNA clone IMAGE:730559 5'	
2816	15368	27837	8.38	4.0E-11 BE863800.1	EST HUMAN	60150731F1 NIH MGCC 71 Homo sapiens cDNA clone IMAGE:3908295 5'	
2897	15613	28083	1.17	4.0E-11 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
4725	17506	28750	0.83	4.0E-11 D44988.1	EST HUMAN	HUMSUPY068 Human brain cDNA Homo sapiens cDNA clone 068	
6802	19198	32005	3.5	4.0E-11 P20085	SWISSPROT	PRE-mRNA SPLICING FACTOR RNA HELICASE PRP2	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7409 19934				4.08	4.0E-11 AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
83116 21830				1.44	4.0E-11 BE148425.1	EST_HUMAN	RC1-HT0286-210100-013-08 HT10286 Homo sapiens cDNA
9580 22080		35045	0.91	4.0E-11 AJ608783.1	EST_HUMAN	CE003855;	882612X1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
12275 24479		30837	1.35	4.0E-11	11545732 NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	
1539 14130		28880	3.73	3.0E-11	8878077 NT	Mus musculus expressed in non-metastatic cells 2, protein (NM_028) (Nm2e2), mRNA	
4363 16950		147	3.0E-11	AA308248.1	EST_HUMAN	EST180120 Liver, hepatobcellular carcinoma Homo sapiens cDNA 5' end	Q3604.X1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1762102 3' similar to contains MER10.1
895 13607		28121	1.84	2.0E-11	AI150502.1	EST_HUMAN	MER10 repetitive element;
1227 13823		28342	5.04	2.0E-11	R24807.1	EST_HUMAN	Y843612.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1227 13826		28343	5.04	2.0E-11	R24807.1	EST_HUMAN	Genus galus (bo-globin, beta-H globin, beta-A globin, epsilon-globin, and deltafactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1655 14247		28780	8.04	2.0E-11	L17432.1	NT	Genus galus (bo-globin, beta-H globin, beta-A globin, epsilon-globin, and deltafactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1655 14247		28781	8.04	2.0E-11	L17432.1	NT	Q51610.X1 Soares, pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gbl028322 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.H1
1659 14252		28786	1.09	2.0E-11	AI128371.1	EST_HUMAN	L1 repetitive element;
3220 15842		28323	0.89	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3368 15978		28453	0.78	2.0E-11	AI478817.1	EST_HUMAN	Im54cd9X1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2161836 3'
3409 16018		28467	0.65	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLYGALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
3544 16148				1.01	2.0E-11 AF020503.1	NT	
4529 17123				0.89	2.0E-11 BE085597.1	EST_HUMAN	RC3-BT0316-170260-014-005 BT0316 Homo sapiens cDNA
4711 17223				0.85	2.0E-11 AI163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5070 17843				1.37	2.0E-11 BE082558.1	EST_HUMAN	QV2-BT0258-281098-014-001 BT0258 Homo sapiens cDNA
6264 18822		31681	1.2	2.0E-11	AW877808.1	EST_HUMAN	QV2-BT0073-288300-109-H08 PT0073 Homo sapiens cDNA
6452 18053							ne83h05.1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR18_YEAST
7246 19773		32832	0.78	2.0E-11	Bf592845.1	EST_HUMAN	P15638 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18.;
7823 20356			0.88	2.0E-11	P37072	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9150	21685		1.27	2.0E-11	AF028508.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10184	22878	35671	4.6	2.0E-11	Q13606	SWISSPROT	OLFACTOORY RECEPTOR 51 (OLFACTOORY RECEPTOR-LIKE PROTEIN OLF1)
10409	22903	35698	0.79	2.0E-11	AW855874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10409	22903	35690	0.79	2.0E-11	AW855874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10892	23500	36538	2.41	2.0E-11	AAD353689.1	EST_HUMAN	zr27g02.s1 Soenes_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
10892	23500	36539	2.41	2.0E-11	AAD353689.1	EST_HUMAN	zr27g02.s1 Soenes_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11805	252020		2.8	2.0E-11	AA704195.1	EST_HUMAN	2177g03.s1 Soenes_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460524 3'
11836	24200		2.49	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
11836	24218	31043	2.26	2.0E-11	BF377559.1	EST_HUMAN	CM2-TN0140-070800-372-d01 TN0140 Homo sapiens cDNA
12136	24388		2.03	2.0E-11	D252172	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12283	24492		5.24	2.0E-11	PF08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12626	24707		3.57	2.0E-11	11417886	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13325	25612	2.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCQ gene locus
816	13434	25639	0.84	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1259	13856	26372	2.93	1.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
1546	14138		1.83	1.0E-11	AF118814.1	NT	Homo sapiens PR0078 mRNA, complete cds
2171	14748	27317	2.61	1.0E-11	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
3548	16150	28630	0.83	1.0E-11	BE5004315.1	EST_HUMAN	CM0-BH0105-170300-282-d12 BN0105 Homo sapiens cDNA
4905	17480		0.97	1.0E-11	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5535	18167	30581	15.03	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5897	18617	31953	0.8	1.0E-11	BF7222648.1	EST_HUMAN	7p57d01.x1 NC1_CGAP Pr28 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10,b3
8143	20684	33596	3.16	1.0E-11	4885646	NT	Homo sapiens PHD finger protein 2 (PHF2), mRNA
8517	21050	33979	4.89	1.0E-11	R13174.1	EST_HUMAN	y73d08.s1 Soenes_infant brain cDNA clone IMAGE:28166 5'
8978	21516	34440	1.38	1.0E-11	BF385119.1	EST_HUMAN	QV4-NH1149-250800-423-e03 NH1148 Homo sapiens cDNA
8978	21516	34441	1.38	1.0E-11	BF385119.1	EST_HUMAN	QV4-NH1149-250800-423-e03 NH1148 Homo sapiens cDNA
11167	23874	36721	2.46	1.0E-11	BF880078.1	EST_HUMAN	602154607f1 NIH_HMG_38 [HMG_38] IMAGE:2856977 5'
2879	15585	28975	0.97	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
9713	22211	35184	5.63	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9713	22211	35185	5.63	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9261	21787		1	8.0E-12	BE074720.1	EST_HUMAN	IL6-BT0578-130200-038-G12 BT0578 Homo sapiens cDNA
11911	24249		4.51	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4766	17347	28798	1.88	7.0E-12	Q05804	SWISSPROT	34 kD SPICULE MATRIX PROTEIN PRECURSOR (LSMK4)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	23759	36815	12.18	7.0E-12 AA704735.1	EST_HUMAN	J223g1.11 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4511523'	
3601	18205		0.72	6.0E-12 AV730554.1	EST_HUMAN	AY730554 HTF Homo sapiens cDNA clone HTFAWF08_5	
4440	17026	28468	10.25	6.0E-12 AA732516.1	EST_HUMAN	nz8811.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Ali repetitive element;	
89226	21484	34380	0.92	6.0E-12 AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds	
9395	21818		1.8	6.0E-12 AA847698.1	EST_HUMAN	cd10g11.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER29.12 MER29 repetitive element;	
1081	13686	26198	2.85	5.0E-12 T06573.1	EST_HUMAN	EST04462 Fetal brain, Striatome (cat#36208) Homo sapiens cDNA clone HFBDV33	
9437	18045	28528	1.19	5.0E-12 BE047778.1	EST_HUMAN	I24205.51 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:22812175'	
3790	16380	28855	6.60	5.0E-12 AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2	
6172	18784	31550	5.50	5.0E-12 AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
6172	18784	31551	5.50	5.0E-12 AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
9817	19214	32019	9.62	5.0E-12 AW974780.1	EST_HUMAN	EST388850 MAGE: resequences, MAGN Homo sapiens cDNA	
7089	19448	32264	1.12	5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_51 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434B16153'	
7108	19448	32284	1.14	5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_51 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434B16153'	
8171	20712	33629	1.43	5.0E-12 AA033745.1	EST_HUMAN	2f01912.51 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:3757183' similar to contains L1.13.1 repetitive element;	
8802	21141		0.7	5.0E-12 AW887037.1	EST_HUMAN	RC1-OT0088-220300-011-b07 OT0088 Homo sapiens cDNA	
8825	21483		0.56	5.0E-12 AL078981.1	EST_HUMAN	DKFZp434J0426_71 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434J0426 5'	
90337	21574	34504	2.42	5.0E-12 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2	
8344	21858	34806	1.04	5.0E-12 P34982	SWISSPROT	OLFACRYORY RECEPTOR 1D2 (OLFACRYORY RECEPTOR-LIKE PROTEIN HGMPO7E) (OLFACRYORY RECEPTOR 17-4) (OR17-4)	
10176	22671		4.17	5.0E-12 AL1683303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
10268	22761	35748	0.67	6.0E-12 AL16833022	NT	Homo sapiens chromosome 21 segment HS21C102	
10481	22855	35968	2.12	5.0E-12 6978754	NT	Rattus norvegicus Deleted in colorectal cancer (ret_hamalog) (Doc), mRNA	
265	12823	25409	3.53	4.0E-12 AA700328.1	EST_HUMAN	J74g11.51 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4606976 3'	
268	12923	25409	4.43	4.0E-12 AA700328.1	EST_HUMAN	J74g11.51 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4606976 3'	
4727	17308	28752	0.82	4.0E-12 AR888894.1	EST_HUMAN	b28105.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR-Q13539 Q13539 MARINER TRANSPOSEASE ;	
7815	20128		0.7	4.0E-12 BF44540.1	EST_HUMAN	mar211043.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2 MER7 repetitive element;	
6185	20726		2.2	4.0E-12 AF103807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	
8821	21160	34075	1.2	4.0E-12 AB042816.1	NT	Bos taurus Mtc2 mRNA for mitochondrial carrier homolog 2, complete cds	

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10961	23476	36501	4.25	4.0E-12	AJ228043.1	NT	Human sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12180	24416		1.61	4.0E-12	U78927.1	NT	Human sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44) and FTP3 (FTP3) genes, complete cds
644	13267	25744	2.73	3.0E-12	AW341683.1	EST_HUMAN	hd13d01_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:26086377 3' similar to TR014517 O14517 SMRP.;
644	13267	25745	2.73	3.0E-12	AW341683.1	EST_HUMAN	hd13d01_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:26086377 3' similar to TR014517 O14517 SMRP.;
5943	16272	39746	1.18	3.0E-12	AF11168.2	NT	Human sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8316	20857	33783	0.52	3.0E-12	O315453	SWISSPROT	SERINE PROTEASE HEPSIN
90335	21572	34501	0.58	3.0E-12	O315453	SWISSPROT	SERINE PROTEASE HEPSIN
10535	23072	36085	3.28	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10535	23072	36086	3.28	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1683	14285	28820	1.05	2.0E-12	AW802131.1	EST_HUMAN	IL5-U0071-120400-065-605 UM0071 Homo sapiens cDNA
3513	16118	28598	0.67	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Kap6-2), mRNA
4192	16781	28229	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4192	16781	28230	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4512	17096		2.58	2.0E-12	BE003509.1	EST_HUMAN	CMD-BT0281-03-1188-087-603 BT0281 Homo sapiens cDNA
6803	18200		1.54	2.0E-12	AW871897.1	EST_HUMAN	EST7383948 MAGE sequences, MAGL, Homo sapiens cDNA
7227	18758	32613	2.87	2.0E-12	T08169.1	EST_HUMAN	EST108050 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
7382	18808	32773	1.21	2.0E-12	BE173035.1	EST_HUMAN	MFD-HT0569-200400-016-608 HT0569 Homo sapiens cDNA
7858	20168	33055	2.38	2.0E-12	11422228	NT	Human sapiens Ac-like transposable element (ALTE), mRNA
7894	20436		0.8	2.0E-12	AV683827.1	EST_HUMAN	AV683827 GKC Homo sapiens cDNA clone GKCFZB04 5'
8232	21854		2.18	2.0E-12	AF188884.1	NT	Human sapiens putative BIPES syndrome breakpoint region protein gene, complete cds
8898	22393		11.42	2.0E-12	BE165980.1	EST_HUMAN	MFR3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA
10408	22802	35698	0.69	2.0E-12	AJ334130.1	EST_HUMAN	qq9702_x1 Scores_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1631835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
11820	24190		2.46	2.0E-12	AL163263.2	NT	hs20029_x1 NCI_CGAP_G1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18_L1
128	12798	25282	2.78	1.0E-12	AW627874.1	EST_HUMAN	MER18 repetitive element;
2031	14613		1.53	1.0E-12	AJ871728.1	EST_HUMAN	wm51f07_x1 NCI_CGAP_G12 Homo sapiens cDNA clone IMAGE:2436483 3' similar to contains L1_L3 L1 repetitive element.
3108	15721	28191	1.33	1.0E-12	AF000891.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TY2) mRNA, partial cds
3943	18641	28007	38.65	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP300-070 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	16541	28008	38.65	1.0E-12	AUJ132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6121	18798		1.85	1.0E-12	U92828.1	NT	Homo sapiens atada telangiectasia (ATM) gene, complete cds
6182	18802		1.95	1.0E-12	Q872G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0861
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6653	19249	32051	0.7	1.0E-12	AF228843.1	NT	Homo sapiens putative BPFES syndrome breakpoint region protein gene, complete cds
7170	19702	32549	1.74	1.0E-12	AF198844.1	NT	qh86a04_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M198503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.H MER10
7204	19735	32587	9.7	1.0E-12	AI248533.1	EST_HUMAN	qh86a04_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M198503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.H MER10
7204	19735	32588	9.7	1.0E-12	AI248533.1	EST_HUMAN	repetitive element;
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S1A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S813S2
8426	20906	33880	0.54	1.0E-12	U68059.1	NT	TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S1A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S813S2
8839	21178	34098	1.18	1.0E-12	AA782323.1	EST_HUMAN	ec28d05_s1 Strategene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
111723	24130	37154	4.65	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGE mosaics, MAGG Homo sapiens cDNA
11941	24273		1.8	1.0E-12	AI738592.1	EST_HUMAN	w33h08_x1 NCI CGAP_Cat6 Homo sapiens cDNA clone IMAGE:2392095 3'
12087	24890		2.72	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12424	24899		2.02	1.0E-12	AF224889.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4019	16617	28082	0.91	9.0E-13	AB029800.1	NT	(UBC203) genes, complete cds
9519	22019		3.1	9.0E-13	N88653.1	EST_HUMAN	zg26b06_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2838651 3'
748	13398	25880	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
748	13398	25881	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1878	14454	27021	3.95	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (Btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8056	20598	33505	0.88	8.0E-13	AI884398.1	EST_HUMAN	wm31h09_x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8056	20598	33506	0.88	8.0E-13	AI884398.1	EST_HUMAN	wm31h09_x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
10051	22546		2.58	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-E6 ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Smaller (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11609	24052	37117	2.51	8.0E-13 U68060.1	NT		Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6SA2T, TCRBV5S3A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV13S8P, TCRBV6S2A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5SAA2T, TCRBV6SA1, TCRBV23S1A2T, TCRBV12
8178	20717		0.83	7.0E-13 Q86155	SWISSPROT		OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12212	24435		37.61	7.0E-13 BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868613' 5'	
12448	24583		1.71	7.0E-13 Q10473	SWISSPROT		POLYPEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE (PROTEIN-UDP-ACETYLGLUCOSAMINYLTRANSFERASE) (UDP-GALNAc-POLYPEPTIDE-N-ACETYLGLUCOSAMINYLTRANSFERASE) (GALNAc-T1)
2149	14728	27299	6.02	6.0E-13 AL183207.2	NT		Homo sapiens chromosome 21 segment HS21C007
3384	15872		0.78	5.0E-13 R7838.1	EST_HUMAN	y82804.1 Soares placenta Nb2-Hp Homo sapiens cDNA clone IMAGE:145759 5'	
3444	16052		1.84	5.0E-13 AA35773.1	EST_HUMAN	z17812.51 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Ali repetitive element:contains element MER22 repetitive element:	
68558	19535	32359	0.88	5.0E-13 P088983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)	
10739	23284	36279	2.49	5.0E-13 P07313	SWISSPROT	MYTOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	
19038	14493		3.69	4.0E-13 AW378314.1	EST_HUMAN	PM2-HT0224-21088-001-011 HT0224 Homo sapiens cDNA	
2500	15084		1.71	4.0E-13 AF003528.1	NT	Homo sapiens glycan 3 (GPC3) gene, partial cds and flanking repeat regions	
4859	17438		1.03	4.0E-13 AA454054.1	EST_HUMAN	zz48dd7.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:785469 5'	
5774	18389	31113	5.09	4.0E-13 BE1689131.1	EST_HUMAN	PN3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA	
7257	19785	32841	1.07	4.0E-13 AB037750.1	NT	Homo sapiens mRNA for KIAA1320 protein, partial cds	
7807	20120	32897	0.81	4.0E-13 AA431529.1	EST_HUMAN	zw78g12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:0452783	
7705	20214		1.84	4.0E-13 NA4201.1	EST_HUMAN	G452783 COR1 mRNA :	
8775	21314	34296	0.94	4.0E-13 AL043010.1	EST_HUMAN	yy63g05.11 Soares melanocyte 2N1HIM Homo sapiens cDNA clone IMAGE:273080 5' similar to PR-A32895	
8833	22420	35403	4.28	4.0E-13 AI2869831.1	EST_HUMAN	A32895 1 complex sterility protein - mouse ;	
11046	23559	38595	1.91	4.0E-13 AA435819.1	EST_HUMAN	DKFZp434A0128_11_434 (synonym: hbsc3) Homo sapiens cDNA clone IMAGE:DKFZp434A0128 5'	
11046	23559	38596	1.91	4.0E-13 AA435819.1	EST_HUMAN	cp32605_x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1890945 3' similar to contains Ali repetitive element:	
192	12852		4.5	3.0E-13 AF003528.1	NT	z178g10.51 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'	
898	13512		4.67	3.0E-13 AA430310.1	EST_HUMAN	Homo sapiens X-linked arthritrophic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
2408	14976	27550	1.06	3.0E-13 AJ2711736.1	NT	zw68g08.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'	
2519	15083		6.72	3.0E-13 AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2687	15245	27812	2.75	3.0E-13	BF372982.1	EST_HUMAN	CN3-FT0100-140700-242-l08 FT0100 Homo sapiens cDNA
3221	16833		3.1	3.0E-13	AA745944.1	EST_HUMAN	db18002.51 NCI CGAP K85 Homo sapiens cDNA clone IMAGE::13240353'
3551	16155	28637	1.04	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3551	16155	28638	1.04	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5730	18356	31060	0.7	3.0E-13	AA134017.1	EST_HUMAN	zr85h10.1r1 Stratogene lung carcinoma 857218 Homo sapiens cDNA clone IMAGE::5653155' similar to zr85h11.1r1 Stratogene lung carcinoma 857218 Homo sapiens cDNA clone IMAGE::5653155' similar to zr85h11.1r1 Stratogene lung carcinoma 857218 Homo sapiens cDNA clone IMAGE::5653155' similar to TR:075139 contains THR.12 THR repetitive element;
5730	18356	31061	0.7	3.0E-13	AA134017.1	EST_HUMAN	contains THR.12 THR repetitive element;
6143	18757	31515	0.68	3.0E-13	AW0056339.1	EST_HUMAN	W788c022x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE::2565890 3' similar to TR:075139
7824	20360	33274	9.59	3.0E-13	U521112	NT	Home sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8021	20563	33464	0.68	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to serine protease P100, reactive factor
8021	20563	33465	0.68	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to serine protease P100, reactive factor
10556	23092		4.07	3.0E-13	AJ084768.1	EST_HUMAN	HA0536 Human fetal liver cDNA Library Homo sapiens cDNA
10624	23443	38464	2.81	3.0E-13	BE063509.1	EST_HUMAN	CN6-8T0281-031198-087-003 BT0281 Homo sapiens cDNA
11469	23919	36968	2.49	3.0E-13	AL165248.2	NT	Home sapiens chromosome 21 segment HS21C048
161	12824	25312	2.58	2.0E-13	U521112	NT	Home sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
260	12819	25406	2.22	2.0E-13	U223839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1313	13907	28427	8.84	2.0E-13	AF239710.1	NT	Home sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3038	15654	28133	0.58	2.0E-13	8924119	NT	Home sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3038	16654	28134	0.68	2.0E-13	8924119	NT	Home sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3320	15930	28407	1.2	2.0E-13	BF431899.1	EST_HUMAN	nsb7605.X1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE::3'
3555	16159	28642				NT	Home sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4188	16776					NT	Home sapiens chromosome 21 segment HS21C078
6271	18879	31647	5.27	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6905	19839	32475	7.42	2.0E-13	X168912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
10355	22849	35843	4.58	2.0E-13	5031898	NT	Homo sapiens mb-21 (C. elegans)-like 1 (MAB21L1) mRNA
11883	24238		20.31	2.0E-13	AW822155.1	EST_HUMAN	CMD-NN0001-100300-274-011 N0001 Homo sapiens cDNA
313	12987	25455	1.6	1.0E-13	S74128.1	NT	FGF-1-fibroblast growth factor 1 [Human, Kidney, Genomic, 342 nt, segment 2 of 2]
921	13594	28052	4.35	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1381	13974	28502	1.01	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-21, IIP2, LMP2, TAP1, LMP7, TAP2, DQB2 and RING8, 9, 13 and 14 genes
2083	14648	27220	1.6	1.0E-13	AA720574.1	EST_HUMAN	THR repetitive element; rw21g02.s1 NCI_CGAP_GCB80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR, 13
4116	16710		2.21	1.0E-13	AA324394.1	EST_HUMAN	EST72725 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing L1 repeat
4686	17278	28724	1.61	1.0E-13	BF340887.1	EST_HUMAN	602038006F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185886 5'
7851	20383	33286	0.77	1.0E-13	AA577812.1	EST_HUMAN	rn24d01.s1 NCI_CGAP_Ges1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains AU repetitive element; contains element MER24 repetitive element;
7851	20383	33297	0.77	1.0E-13	AA577812.1	EST_HUMAN	rn24d01.s1 NCI_CGAP_Ges1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains AU repetitive element; contains element MER24 repetitive element;
10002	22497		0.9	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (NAGE-B4 ANTIGEN)
10202	22897	35891	0.52	1.0E-13	AF200701.1	NT	745e10.x1 Scarecs_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
11258	23780	36842	15.07	1.0E-13	BF108755.1	EST_HUMAN	AV715377 DC8 Homo sapiens cDNA clone DCBAIE03 5'
11714	24124		1.87	1.0E-13	AV715377.1	EST_HUMAN	Hom sapiens Xq pseudoautosomal region; segment 112
12293	24553		4.28	1.0E-13	AJ271735.1	NT	sp24cd1.s1 Scarecs_nht Homo sapiens cDNA clone 1391232 3' similar to contains MER10.11 MER19 repetitive element;
355	13004	25488	4.61	9.0E-14	AA781159.1	EST_HUMAN	sp24cd1.s1 Scarecs_nht Homo sapiens cDNA clone 1391232 3' similar to contains MER10.11 MER19 repetitive element;
356	13005	25489	2.07	9.0E-14	AA781159.1	EST_HUMAN	sp24cd1.s1 Scarecs_nht Homo sapiens cDNA clone 1391232 3' similar to contains MER10.11 MER19 repetitive element;
2545	15109		3.84	9.0E-14	AW881577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2627	15189	27757	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2627	15189	27758	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2782	15335	27985	3.29	9.0E-14	AB0338162.1	NT	Homo sapiens TFF gene cluster for trichill factor, complete cds
3145	15759	28225	4.32	9.0E-14	AW513288.1	EST_HUMAN	aa654h05.x1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3'
3275	13004	25498	0.71	9.0E-14	AA781159.1	EST_HUMAN	aj24cd1.s1 Scarecs_nht Homo sapiens cDNA clone 1391232 3' similar to contains MER10.11 MER19 repetitive element;
3883	18464	28928	7.24	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4870	17446	28887	1.77	9.0E-14	AJ002153.1	NT	Sequinus oedipus gene for seminal vesicle secreted protein semanogelin I

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Table 4
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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3545	16149			0.97	8.0E-14 BE_468263.1	EST_HUMAN	hz71c09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4029	16627			3.29	8.0E-14 R762289.1	EST_HUMAN	yf72c03.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
53369	203698	33211		36.57	8.0E-14 X98211.1	NT	H.sapiens DNA for endogenous retroviral like element
9479	21878	34825		4.61	8.0E-14 AA218316.1	EST_HUMAN	zq17c10.s1 Strategene fetal retina 837292 Homo sapiens cDNA clone IMAGE:628870 3'
11310	23863			4.45	8.0E-14 BE062258.1	EST_HUMAN	QV2-BT0258-261089-014-01 BT0258 Homo sapiens cDNA
12106	24368	308972		2.07	8.0E-14 AI688118.1	EST_HUMAN	wc92b08.x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328143 3'
1671	15447			2.78	7.0E-14 AW154673.1	EST_HUMAN	xf67e10.x1 NCI CGAP_Gass4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.2
88551	21380			0.54	7.0E-14 AL1683285.2	NT	MER10 repetitive element;
390	13036	26526		14.21	6.0E-14 AF020503.1	NT	Homo sapiens chromosome 21 segment HS21 C085
9736	222234	35212		3.27	6.0E-14 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9738	222234	35213		3.27	6.0E-14 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
646	132689	25747		5.26	5.0E-14 Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5209	17774	30197		1.53	5.0E-14 AW073781.1	EST_HUMAN	ab03b05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5724	18350	31053		4.91	5.0E-14 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG repetitive element;
1162	15434			1.61	4.0E-14 P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1920	14505	27062		3.86	4.0E-14 AJ007973.1	NT	Homo sapiens LGMD2B gene
3816	18416			0.84	4.0E-14 AA0468502.1	EST_HUMAN	zd67ea06.r1 Scores_pregnant uterus_NIBI/PU Homo sapiens cDNA clone IMAGE:487858 5'
4378	18986	28412		0.9	4.0E-14 NA6326.1	EST_HUMAN	yf73c12.s1 Scores_multiple_scleroses_2NIBMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
7899	20441			0.49	4.0E-14 X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQB2 and RING3, q, 13 and 14 genes
11633	24073	37135		1.91	4.0E-14 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12457	25107			4.37	4.0E-14 AR888224.1	EST_HUMAN	wm08cd3.x1 NCI CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
985	13587	26110		1.28	3.0E-14 X95468.1	NT	R_norvegicus mRNA for GPC2 protein
5059	17632	30075		0.74	3.0E-14 AW285354.1	EST_HUMAN	xp45f12.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element contains element MER9 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6832	18422	32237	1.08	3.0E-14	AI420788.1	EST_HUMAN	bs91c12x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
6832	18422	32238	1.08	3.0E-14	AI420788.1	EST_HUMAN	bs91c12x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
8722	24281	34181	0.98	3.0E-14	N42165.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ; Y07510_1l1 Soares melanocyte 2N1H M Homo sapiens cDNA clone IMAGE:270523 5'
10872	23393	36403	2.75	3.0E-14	BE888016.1.	EST_HUMAN	601511590F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11116	17832	30075	9.84	3.0E-14	AW28584.1	EST_HUMAN	XP45f12x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains AU repetitive element; contains element MER9 repetitive element ;
12369	24984		1.84	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
413	13048	25539	2.51	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudoeutosomal region; segment 2/2
413	13048	25540	2.51	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudoeutosomal region; segment 2/2
719	15422	25828	9.8	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2431	14898		1.48	2.0E-14	AW372988.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2504	15068		1.07	2.0E-14	7657526	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2567	15131	27699	1.03	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2889	15256		0.88	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5715	18341	30847	0.95	2.0E-14	BF380681.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5804	18429	31148	0.8	2.0E-14	AJ312251.1	EST_HUMAN	bs78h01-32 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5895	18517	31242	2.88	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6883	18640		0.88	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-01-a08 BN0072 Homo sapiens cDNA
7329	18856	32719	1.12	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7518	20038	32906	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0387-071289-024-D04 HT0387 Homo sapiens cDNA
7518	20038	32907	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0387-071289-024-D04 HT0387 Homo sapiens cDNA
8831	22329	35311	0.54	2.0E-14	AJ878785.1	EST_HUMAN	wr5gj10_x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2482034 3' similar to contains AU repetitive element;
10859	23191	36206	4.65	2.0E-14	AW139800.1	EST_HUMAN	UH-B11-adv-a-10-0-U1,s1 NCI_CGAP_SuS3 Homo sapiens cDNA clone IMAGE:2718234 3'
12368	24988		3.3	2.0E-14	AF008191.1	NT	Home sapiens putative G6 protein (G6P) gene, complete cds
12617	15068		1.99	2.0E-14	7657529	NT	Home sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1106	13709	28218	1.89	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1452	14044	28572	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1452	14044	28573	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2044	14626	27195	7.63	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2228	14803	27374	5.33	1.0E-14	AL1633393.2	NT	Homo sapiens chromosome 21 segment HS21C103
2453	15020	27591	5.89	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2971	15587	28069	1.51	1.0E-14	PO5227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-1)
3203	15815	28290	3.91	1.0E-14	BF3365227.1	EST_HUMAN	RC2-CT0432-310700-013-009_1 CT0432 Homo sapiens cDNA
3203	15815	28291	3.91	1.0E-14	BF3365227.1	EST_HUMAN	RC2-CT0432-310700-013-009_1 CT0432 Homo sapiens cDNA
3955	16553	28022	2.1	1.0E-14	AA862994.1	EST_HUMAN	aa89e12.51 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:2753059 3'
4572	17155	29590	1.71	1.0E-14	AW2753522.1	EST_HUMAN	xq39h10.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5977	18597	31332	2.03	1.0E-14	AF120145.1	NT	Bos taurus zearibofatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6778	24770	32183	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6778	24770	32184	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1620	14213	28744	1.19	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2217	14782		1.39	9.0E-15	AF180778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JH5 protein, JHA protein, T54 protein, JH10 protein, AA differentiation-dependent protein, triple LIM domain, protein 6, and synaptophysin genes, complete cds; and L-type calcium channel &
7507	20020	32892	3.77	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7859	20501	33410	1.38	9.0E-16	BE803550.1	EST_HUMAN	601677750F1 NIH_MCG_21 Homo sapiens cDNA clone IMAGE:3980166 6'
12580	24680		1.76	9.0E-15	AL1633247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2837	13138		1.17	8.0E-15	BE281482.1	EST_HUMAN	601148632F1 NIH_MCG_19 Homo sapiens cDNA clone IMAGE:3184023 5'
7233	19733	32819	1.29	7.0E-15	BF036327.1	EST_HUMAN	601458331F1 NIH_MCG_68 Homo sapiens cDNA clone IMAGE:3862088 5'
10331	22825		2.53	7.0E-15	AW241958.1	EST_HUMAN	xq77d92.21 Scans_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to gtl21834 STEROL THR12 TIR repetitive element :
11778	24164		1.78	7.0E-15	AA284465.1	EST_HUMAN	2557d98.1M NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gtl21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1 H L1 repetitive element ;
1031	13641	26150	6.29	6.0E-15	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
6077	18894	31440	1.18	6.0E-15	X73462.1	NT	O-series mRNA for hair keratin cysteine-rich protein
6077	18894	31441	1.18	6.0E-15	X73462.1	NT	O-series mRNA for hair keratin cysteine-rich protein
11182	25128		1.86	6.0E-15	AW636843.1	EST_HUMAN	QV1-LTD036-150200-070-c10 LT0036 Homo sapiens cDNA
12648	24722		1.3	6.0E-15	BF432200.1	EST_HUMAN	nb81c12.X1 Scans_NSF_F8_9N_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2731219 3'
435	13068	25563	5.19	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2789	18342	27912	2.35	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Reret gene, and sodium phosphate transporter (NPT3) gene, complete cds
3515	16120		1.06	5.0E-15	AW298817.1	EST_HUMAN	U1-H-BW0-4B-9-10-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]							
5289 17891			1.28	5.0E-15 P11389		SWISSPROT	
10555 23091			2.72	5.0E-15 AV73056.1	EST_HUMAN	AV73056 HTF Homo sapiens cDNA clone HTFAVE08 5'	
452 12881	25137		2.33	4.0E-15 AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
6771 18284	32173		0.78	4.0E-15 AB001970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501	
10840 20287	33184		2.54	4.0E-15 AJ303894.1	NT	Homo sapiens mRNA for transcription factor	
10840 20287	33185		2.54	4.0E-15 AJ303894.1	NT	Homo sapiens mRNA for transcription factor	
4287 18883			7.28	3.0E-15 N88482.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to LY1142 5 similar to ANF(CARDIAC) LATION)	
5060 17833			0.57	3.0E-15 PQ2485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5	
5178 17748	30175		0.72	3.0E-15 AA078097.1	EST_HUMAN	TP01FC03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone TP01FC03	
5179 17748	30178		0.72	3.0E-15 AA078097.1	EST_HUMAN	TP01FC03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone TP01FC03	
68904 18838			1.41	3.0E-15 Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)	
7323 18850	32711		3.48	3.0E-15 M277885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds	
7323 18850	32712		3.48	3.0E-15 M277885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds	
9839 22337			2.32	3.0E-15 AA807128.1	EST_HUMAN	oc3Ba07_s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351784 3' similar to contains MER19.11 MER19 repetitive element :	
10073 23205	36218		3.36	3.0E-15 AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)	
12114 24897			1.38	3.0E-15 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2	
271 12828	25415		4.1	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
391 13037	26526		3.78	2.0E-16 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
391 13037	25527		3.78	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
2410 14878	27552		1.44	2.0E-15 BE350127.1	EST_HUMAN	ht08g011_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER20.13 MER29 repetitive element :	
2410 14878	27553		1.44	2.0E-15 BE350127.1	EST_HUMAN	ht08g011_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER20.13 MER29 repetitive element :	
3559 16163	28845		0.73	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
3559 16163	28848		0.73	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4142	16734	29188	0.95	2.0E-15 AW238489.1	EST_HUMAN	xp28n01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741821 3' similar to contains L1.13 L1 repetitive element;	
4729	17310		2.72	2.0E-15 AI808395.1	EST_HUMAN	W0708.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR:Q861043 Q81043 NINEIN.;	
5332	17893	30306	0.93	2.0E-15 P139893	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR	
5332	17893	30307	0.93	2.0E-15 P139893	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR	
6329	18935	31711	1.02	2.0E-15 BE582352.1	EST_HUMAN	601344253F1 NIH_MCG_B Homo sapiens cDNA clone IMAGE:3677268 5'	
6329	18935	31712	1.02	2.0E-15 BE582352.1	EST_HUMAN	601344253F1 NIH_MCG_B Homo sapiens cDNA clone IMAGE:3677268 5'	
7168	19700		1.37	2.0E-15 AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene	
7315	19842	32703	2.51	2.0E-15 AA704195.1	EST_HUMAN	2177603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4608243'	
7427	19951	32816	4.49	2.0E-15 W05084.1	EST_HUMAN	21776d10.r1 Soares_fetal_lung_NiHL19W Homo sapiens cDNA clone IMAGE:288875 5' similar to WP:F44F.8 CE022277 TRANSPPOSEASE.;	
8837	21378	34300	2.62	2.0E-15 D14547.1	NT	Human DNA, SINE repetitive element	
9002	21539	34468	0.87	2.0E-15 AA397758.1	EST_HUMAN	2177608.r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:72B4145	
9002	21539	34469	0.87	2.0E-15 AA397758.1	EST_HUMAN	2177608.r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:72B4145	
9325	21839	34780	1.13	2.0E-15 AW370485.1	EST_HUMAN	CMD-HT0244-201089-078-a12 HT0244 Homo sapiens cDNA	
9325	21839	34781	1.13	2.0E-15 AW379485.1	EST_HUMAN	CMD-HT0244-201089-078-a12 HT0244 Homo sapiens cDNA	
10719	23246		3.59	2.0E-15 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2	
12487	16163	28845	2.97	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced	
12487	16163	28846	2.97	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced	
2803	15355		2.08	1.0E-15 AI888984.1	EST_HUMAN	b28n05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13639 MARINER TRANSPOSEASE.;	
3048	156932	28143	1.24	1.0E-15 BE043584.1	EST_HUMAN	1K40d02.v1 NCI_CGAP_Ox34 Homo sapiens cDNA clone IMAGE:2889162 5'	
3178	16789	28281	1.05	1.0E-15 P08547	SWISSPROT	L1NE-1 REVERSE TRANSCRIPTASE HOMOLOG	
6510	19110	31898	1.71	1.0E-15 T05763.1	EST_HUMAN	y40s10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element.	
7080	19852		1.91	1.0E-15 BED74217.1	EST_HUMAN	QV3-BT0558-270100-074-g05 BT0589 Homo sapiens cDNA	
7105	19445	32282	0.77	1.0E-15 P39057	SWISSPROT	DYNEIN BETA CHAIN, CILLARY	
8174	20715	33631	0.89	1.0E-15 AL163230.2	NT	Homo sapiens chromosome 21 segment HS21C080	
8359	20890	33819	4.97	1.0E-15 AI200978.1	EST_HUMAN	q88g08.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1765227 3'	
8359	20890	33820	4.97	1.0E-15 AI200978.1	EST_HUMAN	q88g08.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1765227 3'	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8968	21507	34428	0.51	1.0E-15	AL163207.2	NT		Homo sapiens chromosome 21 segment HS21C007
8972	21510	34432	1.89	1.0E-15	4507208	NT		Homo sapiens spermidine synthase (SRM) mRNA
9171	21748	34681	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	
9550	22050	35012	1.18	1.0E-15	AA884653.1	EST_HUMAN		dt3703_s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:14689723' similar to contains L1.13 L1 repetitive element;
10888	23228	36242	6.88	1.0E-15	AF044083.1	NT		Homo sapiens major histocompatibility locus class III region
12684	24820	30782	9.35	1.0E-15	AI783944.1	EST_HUMAN		lt31cc5_s1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:22189123' similar to contains Alu repetitive element,
4417	170702		0.63	9.0E-16	BF069497.1	EST_HUMAN		602120192F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277422 5'
4602	17185	29832	1.11	9.0E-16	4503168	NT		Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CU1TL1) mRNA
10973	22394	38406	2.68	9.0E-16	FD08888.1	EST_HUMAN		HSC28F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23Fr5
5880	18502	31228	0.73	7.0E-16	4885120	NT		Homo sapiens chemotactin (C-C motif) receptor 8 (CCR8) mRNA
7379	18905	32789	1.38	7.0E-16	O88807	SWISSPROT		PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7379	18905	32770	1.38	7.0E-16	O88807	SWISSPROT		PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12559	24916		33.75	7.0E-16	TD9140.1	EST_HUMAN		ye28c12/r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:1190062 5'
2188	14762		28.28	8.0E-16	AW972811.1	EST_HUMAN		EST384702 MAGE sequences, MAGL, Homo sapiens cDNA
5436	17981	30397	0.94	8.0E-16	BF385702.1	EST_HUMAN		QV2-NT0048-160800-316-d12 NT0048 Homo sapiens cDNA
1539	14131	28887	1.21	5.0E-16	AJ251154.1	NT		Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2705	15262	27829	2.6	5.0E-16	AA882178.1	EST_HUMAN		ct80cp4_s1 Scores_low_fetus_Nb2H-F8_9W Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11398	23848	36914	3.78	5.0E-16	BF217388.1	EST_HUMAN		contains element L1 repetitive element;
12808	24690		4.98	5.0E-16	11418127	NT		Hom sapiens GTP binding protein 1 (GTPBP1), mRNA
2281	14855		1.23	4.0E-16	AB001528.1	NT		[Hom sapiens gene for TMEM1 and PWP2, complete and partial cds]
2419	14987	27581	1.68	4.0E-16	AW767168.1	EST_HUMAN		QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
2419	14987	27582	1.68	4.0E-16	AW767168.1	EST_HUMAN		QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
3503	16108	28584	6.73	4.0E-16	Q16893	SWISSPROT		MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4223	16811	29258	4.28	4.0E-16	BE083875.1	EST_HUMAN		PIM-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4223	16811	29259	4.28	4.0E-16	BE083875.1	EST_HUMAN		PIM-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
7688	20207	33094	37.48	4.0E-16	AL163284.2	NT		Homo sapiens chromosome 21 segment HS21C0084
9219	21738	34678	1.44	4.0E-16	11423191	NT		Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11098	23808	36846	1.68	4.0E-16	AV730303.1	EST_HUMAN		AV730303 HTF Homo sapiens cDNA clone HTFAWA03 5'

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Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11800	24180			1.34	4.0E-16 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11887	24232			13.76	4.0E-16 C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone b1cc5355
11897	24239	31008		2.91	4.0E-16 6912459	NT	Homo sapiens Gnb2-associated binder 2 (KIAA0571), mRNA
12178	24414			1.8	4.0E-16 R18591.1	EST_HUMAN	Y88511.1 Soenes Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
138	12803	25282		0.83	3.0E-16 AW022882.1	EST_HUMAN	d45c01.1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488378 5'
138	12803	25283		0.83	3.0E-16 AW022882.1	EST_HUMAN	d45c01.1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488378 5'
491	13124			1.24	3.0E-16 AL048445.1	EST_HUMAN	DKFZp434P037_11 434 (synonym: fates3) Homo sapiens cDNA clone DKFZp434P037 5'
501	13133			2.35	3.0E-16 AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1501	14083	26832		1.81	3.0E-16 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3004	16620	28097		4.2	3.0E-16 P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4007	16805	28079		0.61	3.0E-16 T08168.1	EST_HUMAN	EST04060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
4031	16828			1.07	3.0E-16 U03887.1	NT	Human BXP-20 gene
4889	17271	28720		0.97	3.0E-16 AW160828.1	EST_HUMAN	a78608_1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782183 5' similar to SW:KD1 MOUSE Q81751 RENAL TRANSCRIPTION FACTOR KID-1;
5077	17650	30091		1.14	3.0E-16 AV861383.1	EST_HUMAN	AV861383 GLC Homo sapiens cDNA clone GLCGSA01 3'
6482	18118			0.9	3.0E-16 AA077226.1	EST_HUMAN	7810F02 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7B10F02
5801	18428	31144		1.57	3.0E-16 AF083528.1	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
6592	21131	34047		4.08	3.0E-16 AI002838.1	EST_HUMAN	am88105_s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
8805	22303			0.84	3.0E-16 BF890017.1	EST_HUMAN	602246538F1 NIH MGCG_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10027	22522	35518		5.15	3.0E-16 L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12637	25078	30516		9.33	3.0E-16 AL043268.2	EST_HUMAN	DKFZp434L1623_11 434 (synonym: fates3) Homo sapiens cDNA clone DKFZp434L1623 5'
1007	13818			1.38	2.0E-16 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2429	14886			1.01	2.0E-16 AA021781.1	EST_HUMAN	a00604_a1 Soenes_letsis_NH1 Homo sapiens cDNA clone IMAGE:1030835 3'
2713	15270			1.53	2.0E-16 J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4257	16843	28292		1.34	2.0E-16 X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
5370	17830	30344		0.57	2.0E-16 BE061178.1	EST_HUMAN	RC3-BT048-131189-003-H12 BT046 Homo sapiens cDNA
6839	19429	32245		0.80	2.0E-16 Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7701	20210	S3097		0.76	2.0E-16 AI470723.1	EST_HUMAN	Y18611_x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
7808	20450	33357		1.81	2.0E-16 A1732837.1	EST_HUMAN	#24708_x6 NC1 CGAP_Pt12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:054849 O54849 HYPOTHETICAL_42.9_KD PROTEIN. [2] TR:008805 :contains MER7.11 MER7 repetitive element ;

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Probe Seq ID No:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8099	20640	33551	0.7	2.0E-10	BE858028.1	EST_HUMAN	7782b09_x1 NCI_CGAP_P-728 Homo sapiens cDNA clone IMAGE-3303621 3'
8099	20640	33552	0.7	2.0E-10	BE858028.1	EST_HUMAN	7782b09_x1 NCI_CGAP_P-728 Homo sapiens cDNA clone IMAGE-3303621 3'
8464	21004	33921	0.6	2.0E-10	AW877214.1	EST_HUMAN	CMA-PT0034-180200-506-001 PT0034 Homo sapiens cDNA
8464	21004	33922	0.6	2.0E-10	AW877214.1	EST_HUMAN	CMA-PT0034-180200-506-001 PT0034 Homo sapiens cDNA
10808	23331	38343	2.71	2.0E-16	6902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
197	12857	25339	2.56	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds af359g11_s1 Scars_telo_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE-1034084 3' similar to contains OFR.12 OFR repetitive element;
405	13080		20.83	1.0E-16	AA626592.1	EST_HUMAN	QV0-BN0148-070700-283-010 BN0148 Homo sapiens cDNA
2014	14598	27159	1.78	1.0E-16	BF3277942.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds; alternatively spliced
5898	18518	31243	0.85	1.0E-16	AF163884.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6565	19+63		27.68	1.0E-16	U45693.1	NT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6888	18284	32087	2.77	1.0E-16	Q02779	SWISSPROT	
7558	19163		6.88	1.0E-16	U45693.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9207	21724	34687	1.15	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-005 PT0012 Homo sapiens cDNA
3802	18402	28866	2.48	9.0E-17	AW800048.1	EST_HUMAN	CM1-NN1003-200300-153-001 NN1003 Homo sapiens cDNA tg22c11_x1 NCI_CGAP_CIL1 Homo sapiens cDNA clone IMAGE-2109524-3' similar to contains MER28.12
6824	18414		1.94	9.0E-17	A1392984.1	EST_HUMAN	MER28 repetitive element;
8052	20594		4.85	9.0E-17	AW150257.1	EST_HUMAN	xg48g12_x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE-26309850 3' similar to contains OFFR.12 OFFR repetitive element;
10124	22819		2.1	8.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1058	13881		1.59	8.0E-17	AW880701.1	EST_HUMAN	QV0-O-T0032-080308-155-001 O10032 Homo sapiens cDNA
38981	16859		0.7	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5771	24748	31111	3.65	8.0E-17	BE172081.1	EST_HUMAN	MRD-HT0558-080300-003-004 HT0558 Homo sapiens cDNA
7319	18846		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1505	14097		3.4	7.0E-17	67530897	NT	Mus musculus apolipoprotein B editing complex 2 (Apobec-2), mRNA
5528	18158		2.67	7.0E-17	AF216850.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds; alternatively spliced
6789	18380	32198	7.15	7.0E-17	AF228943.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
217	12878	25385	7.43	6.0E-17	AW883880.1	EST_HUMAN	RC1-HN003-220300-021-004 HN003 Homo sapiens cDNA
6455	18058	31841	1.68	6.0E-17	AW882772.1	EST_HUMAN	h181d04_x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-2878885 3' similar to contains L1.12 L1 repetitive element;
10182	22887	35680	0.52	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87)

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Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	12875	25131	2.78	5.0E-17	T8410.1	EST_HUMAN	y05n08_r1 Stratagene lung (4837210) Homo sapiens cDNA clone IMAGE:78839 5'
7589	20101	32870	1.82	5.0E-17	T81043.1	EST_HUMAN	yd28604_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108327 5'
8284	21884	34829	1.12	4.0E-17	AW128165.1	EST_HUMAN	xf20804_x1 NCI_CGAP_KidB Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Atu repetitive element;contains MER19.b1 MER19 repetitive element;
11365	23817	36878	2.17	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1818	24188		2.38	4.0E-17	AI073548.1	EST_HUMAN	0415604_x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1540	14132		1.03	3.0E-17	D14547.1	NT	Human DNA_SINE repetitive element
2146	14723	27295	1.28	3.0E-17	AW118123.1	EST_HUMAN	xd88909_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3227	15839		1.41	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3704	16305	28773	1.24	3.0E-17	BE328522.1	EST_HUMAN	tw05b04_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
3704	16305	28774	1.24	3.0E-17	BE328522.1	EST_HUMAN	tw05b04_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
5181	17747		1.02	3.0E-17	BF511288.1	EST_HUMAN	UI-H-B14-asj-c-08-0-LJL_s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30885043 3'
8212	20753	33887	1.09	3.0E-17	N88451.1	EST_HUMAN	za14002_x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282461 3' similar to contains PTR5_x3 PTR5 repetitive element;
8618	22118	36081	4.54	3.0E-17	AB028888.1	NT	Homo sapiens DNA_DLE1 to ORCCTL4 gene region, section 1/2 (DLE1, ORCCTL3, ORCCTL4 genes, complete cds)
10282	22777	35787	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-0112 BN0047 Homo sapiens cDNA
10282	22777	35788	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-0112 BN0047 Homo sapiens cDNA
11776	24163		3.77	3.0E-17	11417888	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
375	13024	25510	3.38	2.0E-17	A1270080.1	EST_HUMAN	qf63308_x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1858822 3' similar to contains Atu repetitive element;
378	13024	25510	2.68	2.0E-17	A1270080.1	EST_HUMAN	qf63308_x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1858822 3' similar to contains Atu repetitive element;
1025	13836		1.12	2.0E-17	AA722632.1	EST_HUMAN	zg81d0_x1 Soares_fetal_heart_NbH18W Homo sapiens cDNA clone IMAGE:389751 3'
2490	15055	27627	2.43	2.0E-17	Q28893	SWISSPROT	ZONADHESIN PRECURSOR
2490	15055	27628	2.43	2.0E-17	Q28893	SWISSPROT	ZONADHESIN PRECURSOR
2856	15572	28049	8.08	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 kDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5568	18200	30848	1.57	2.0E-17	W27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5569	18200	30849	1.57	2.0E-17	W27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6410	180113		1.8	2.0E-17	AF056068.1	NT	Homo sapiens MHC class 1 region
6816	19213		1.68	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610_r1 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
7773	20282	33178	0.85	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8028	20570	33474	1.64	2.0E-17	Q95158	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8394	20834	33858	1.15	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
9783	22281	35287	2.45	2.0E-17	BE296988.1	EST_HUMAN	6008444680F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860015 5'
9818	22316	35288	3.98	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9818	22316	35288	3.98	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10160	22655	35680	7.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10281	22778	35785	0.98	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10281	22778	35786	0.98	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10308	22800	35781	0.63	2.0E-17	AI788902.1	EST_HUMAN	web404.xls Saccharomyces_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10308	22800	35782	0.63	2.0E-17	AI788902.1	EST_HUMAN	web404.xls Saccharomyces_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
780	13399	25602	3.98	1.0E-17	P08163	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1748	14388		1.2	1.0E-17	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1804	14394	26838	2.89	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2162	14739	27309	2.11	1.0E-17	PO2461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2373	14943	27616	1.88	1.0E-17	UT8410.1	NT	Homo sapiens transobsondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3625	16228		0.89	1.0E-17	AF224469.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4217	16806	848	1.0E-17	R09942.1	EST_HUMAN	Y303607.1 Saccharomyces cerevisiae fission yeast 1NFLS Homo sapiens cDNA clone IMAGE:1283388 5'	
6759	19352	32161	1.55	1.0E-17	AI165642.1	EST_HUMAN	q6365b05.xls Saccharomyces_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6759	19352	32162	1.55	1.0E-17	AI165642.1	EST_HUMAN	q6365b05.xls Saccharomyces_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7148	19678	32580	1.28	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8528	21067	33986	1.23	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101289-072-407 BT0263 Homo sapiens cDNA
8919	22415	35380	0.94	1.0E-17	AW886538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11285	23747	36805	1.82	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2510	15074	27847	1.13	9.0E-18	AA174078.1	EST_HUMAN	ZP18g12.3 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:6098862 3'
9418	21827		3.03	9.0E-18	AI472167.1	EST_HUMAN	Y886403.xls Saccharomyces_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148398 3'
3854	18452	28915	1.58	8.0E-18	4759877	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
371	13020	25504	32.88	7.0E-18	AW316978.1	EST_HUMAN	xx10b04.xls NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1:208388 90S
371	13020	25505	32.88	7.0E-18	AW316978.1	EST_HUMAN	xx10b04.xls NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1:208388 90S
7468	19891	32854	0.98	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT00091-170300-011-d03 OT0091 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12206 13020	25504	5.28	7.0E-18	AW318978.1	EST_HUMAN	x10b04_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:28370711 3' similar to gb:U20868 80S RIBOSOMAL PROTEIN L4 (HUMAN);	
12206 13020	25505	5.28	7.0E-18	AW318978.1	EST_HUMAN	x10b04_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:28370711 3' similar to gb:U20868 80S RIBOSOMAL PROTEIN L4 (HUMAN);	
3334 15844	28419	1.39	6.0E-18	X717812	NT	Rattus norvegicus partial GmNP-1 gene for gba-derived neuropeptide neadn 1, enhancer region	
4857 17435		3.95	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)	
8182 20733		2.75	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC33446), mRNA	
8289 20830	33751	0.6	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
11014 23528	36664	1.87	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046	
11209 23713	36767	1.9	6.0E-18	X87344.1	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC830891), mRNA	
11591 24034		2.22	6.0E-18	11428885	NT	Homo sapiens chromosome 21 segment HS21C046	
12041 24328	30985	2.24	6.0E-18	U87829.1	NT	Human ecdonitide hydrolase (ACO2) gene, exon 4	
1187 13788	26289	11.3	5.0E-18	AI280214.1	EST_HUMAN	Qm65g11_X1 Scores_5to9Weeks_2Nt IPSto9W Homo sapiens cDNA clone IMAGE:1883668 3'	
5284 17846	30273	0.94	5.0E-18	D61517.1	EST_HUMAN	similar to contains Alu repetitive element; HUMA11F05B Clontech human fetal brain polyA+ mRNA (#8335) Homo sapiens cDNA clone GEN-411F05 5'	
5477 18111	30520	1.03	5.0E-18	AF087013.1	NT	Human endogenous retrovirus HERV-P-T47D	
88654 21193	34111	4.62	5.0E-18	BE143312.1	EST_HUMAN	MRE-HTT0161-221089-002-008 HTT0161 Homo sapiens cDNA	
10657 23378	36398	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC510888), mRNA	
10657 23378	36397	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC510888), mRNA	
12170 24409		6.6	6.0E-18	AW887182.1	EST_HUMAN	MR1-SN0035-060400-001-911 SN0035 Homo sapiens cDNA	
12531 24844		51.19	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCG3A02 3'	
130 12797	25283	1.98	4.0E-18	BE044076.1	EST_HUMAN	hs36h04_x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2038511 3' similar to contains MER28_b3 MER28 repetitive element;	
130 12797	25284	1.98	4.0E-18	BE044076.1	EST_HUMAN	hs36h04_x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M22328	
1754 14344	26880	8.14	4.0E-18	AA621814.1	EST_HUMAN	rq24f11_x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M22328 KERATIN, TYPE I CYTOSKELELETAL 18 (HUMAN);	
1633 14517		0.82	4.0E-18	AI738592.1	EST_HUMAN	w33h08_x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'	
2242 14817	27390	1.23	4.0E-18	Q08630	SWISSPROT	N-ACETYL-LACTOSAMINIDE BETA-1,6-N-ACETYLGUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYL TRANSFERASE) (BRANCHING ENZYME) (IGNT)	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14817	27391	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINYLTRANSFERASE (N-
55688	18197	30843	2.32	4.0E-18	AI017565.1	EST_HUMAN	ACETYLGLUCOSAMINYLTRANSFERASE (BRANCHING ENZYME) (IGNT)
55689	18197	30844	2.32	4.0E-18	AI017565.1	EST_HUMAN	cu23a08_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:16277138_3'
							cu23a08_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:16277138_3'
7787	20330		0.81	4.0E-18	AA748811.1	EST_HUMAN	mb34a08_s1 NCI_CGAP_Alt1 Homo sapiens cDNA clone IMAGE:12868988 similar to contains L1.t2_L1
10884	23405	36424	7.68	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to SW.RS3_HUMAN
882	13498	26015	18.02	3.0E-18	AA814198.1	EST_HUMAN	cb23h11_31 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW.RS3_HUMAN
885	13578	26091	2.25	3.0E-18	BE088634.1	EST_HUMAN	P48782_40S RIBOSOMAL PROTEIN S5.:
4022	16820	28083	1.23	3.0E-18	AL103247.2	NT	CMD-BT0680-210300-288-907 BT0680 Homo sapiens cDNA
6917	10578	32405	6.68	3.0E-18	BE001871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12312	24504		8.85	3.0E-18	AW022015.1	EST_HUMAN	IPM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
-	272	12829	2.57	2.0E-18	AW836820.1	EST_HUMAN	df81h12_y1 Marfan Fetal Cochlea Homo sapiens cDNA clone IMAGE:24885728_5'
1192	13783		197.1	2.0E-18	BE258097.1	EST_HUMAN	QV14-LT0038-150200-070-a07_LT0038 Homo sapiens cDNA
3157	15771	28238	1.15	2.0E-18	Q339575	SWISSPROT	601114352f1 NIH_MSC_18 Homo sapiens cDNA clone IMAGE:35355044_5'
5606	18235		3.89	2.0E-18	AA888810.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5697	18323	30823	3.16	2.0E-18	D14547.1	NT	8453a07_s1 Scores_Insits_NHT Homo sapiens cDNA clone IMAGE:1408952 3' similar to TR:O14577
							O14577_BAC CLONE RG11A06 FROM 7Q31, COMPLETE SEQUENCE.:
5697	18323	30824	3.16	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
60238	18857		1.88	2.0E-18	BF347229.1	EST_HUMAN	602021184f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158870_5'
63133	18920	31695	1	2.0E-18	X80459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
63133	18920	31696	1	2.0E-18	X80459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6424	18027	31810	0.84	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0018-220700-222-C12 HT0619 Homo sapiens cDNA clone IMAGE:23-HT0018
6460	18061	31847	7.53	2.0E-18	AW888853.1	EST_HUMAN	hr4q01.1x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.2
9880	22455	35437	1.39	2.0E-18	AW151673.1	EST_HUMAN	MER10 repetitive element;
8880	22455	35498	1.39	2.0E-18	AW151673.1	EST_HUMAN	x87610_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.2
10854	23376	36394	4.96	2.0E-18	AW470781.1	EST_HUMAN	mer10 repetitive element;
							ha33d08_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR13
							THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11578	24026	37083		5.24	2.0E-18 AW151269.1	EST_HUMAN	xp47e69.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2830728 3' similar to contains MER8.b2 MER8 repetitive element;
11970	13783			20.18	2.0E-18 BE256097.1	EST_HUMAN	b01114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4507	17091			0.85	1.0E-18 T854081.1	EST_HUMAN	ye43g05.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
55558	18190	30603	1.91	1.0E-18 AV853405.1	EST_HUMAN	AV853405 GLC Homo sapiens cDNA clone Gl_CDKE11 3'	
57559	18385	31093	2.18	1.0E-18 D000989.1	NT	Homo sapiens mRNA for Na-K-ATPase alpha-subunit, complete cds	
57559	18385	31100	2.18	1.0E-18 D000989.1	NT	Homo sapiens mRNA for Na-K-ATPase alpha-subunit, complete cds	
65582	19180	31980	1.37	1.0E-18 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080	
83390	20620	33840	1.22	1.0E-18 AI148288.1	EST_HUMAN	c029d09.x1 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680563 3' similar to contains L1.t1 L1 repetitive element;	
98113	22311	35283	4.45	1.0E-18 U813228.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rnf17 gene, and sodium phosphate transporter (NP73) gene, complete cds	
11918	24255	31011	4.39	1.0E-18 AF003229.1	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions	
571	13202	25684	3.33	9.0E-19 AA281981.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.i2 MER19 repetitive element;	
572	13202	25684	2.88	9.0E-19 AA281981.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.i2 MER19 repetitive element;	
7790	20333			5.83	9.0E-19 F086888.1	EST_HUMAN	HSC23Fc51 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
86222	21161	34076	2.46	9.0E-19 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21 C003	
86222	21161	34077	2.46	9.0E-19 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21 C003	
11007	23521	36856	3.92	9.0E-19 AB032069.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds	
11078	13202	25684	28.32	9.0E-19 AA281981.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.i2 MER19 repetitive element;	
10888	13691		1.38	8.0E-19 AW874902.1	EST_HUMAN	EST387007 MAGN Homo sapiens cDNA	
80890	20631	33544	1	8.0E-19 BE158338.1	EST_HUMAN	MFO-HT04-04-210200-001-g06 HT0404 Homo sapiens cDNA	
2287	14861	27438	1.72	7.0E-19	4758139 NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/Hs) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA	
65584	19182	31982	1.91	7.0E-19 AF092090.1	NT	RetinA nonnegligible cp151 mRNA, partial cds	
7341	18898	32732	0.85	7.0E-19 P28444	SWISSPROT	BETA CRYSTALLIN A2	
98225	22421	35595	0.47	7.0E-19 AI344951.1	EST_HUMAN	b011c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'	
11823	25088		2.85	7.0E-19 AA705684.1	EST_HUMAN	z601b01.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:135145 3'	
3847	16446		1.21	6.0E-19 AW852830.1	EST_HUMAN	PM0-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
4582	17445	28582	1.39	6.0E-19 P34886	SWISSPROT	OLFACTOORY RECEPTOR 6 (M50)		
4582	17445	28583	1.39	6.0E-19 P34886	SWISSPROT	OLFACTOORY RECEPTOR 6 (M50)		
4910	17494		1.15	6.0E-19 AJ271735.1	NT	Homo sapiens Xq presubautosomal region; segment 1/2	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)	
6019	18838	31378	5.29	5.0E-19 Q00193	SWISSPROT			
6365	18839	31747	0.79	5.0E-19 AW683302.1	EST_HUMAN	Hh7750e.y1 NCI_CGAP_Gut Homo sapiens cDNA clone IMAGE:28068707.5		
10322	22816	35812	0.68	5.0E-19 AJ297689.1	NT	Homo sapiens partial IL-12 receptor beta1 chain, exon 14		
11412	23863	36924	7.61	5.0E-19 AW183725.1	EST_HUMAN	#37b02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28841171 3' similar to contains element MSR1 repetitive element;		
12544	24823		1.38	5.0E-19 U68080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S3A2T, TCRBV13S9P, TCRBV6S3A1N1T, TCRBV9S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1.		
580	13210	25889	0.95	4.0E-19 AB007870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501		
2707	15234	27831	1.25	4.0E-19 BF697362.1	EST_HUMAN	#6021308910F1 NIH_MGIC_56 Homo sapiens cDNA clone IMAGE:42876745'		
5583	18223	30672	1.1	4.0E-19 AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds		
3919	186117	28982	1.58	3.0E-19 Q288897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR		
3919	186117	28983	1.58	3.0E-19 Q288897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR		
4373	16880	28405	0.9	3.0E-19 O43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)		
4373	16880	28406	0.9	3.0E-19 O43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)		
4544	17128	28571	1.33	3.0E-19 AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADAMA11 5'		
6484	18118		0.8	3.0E-19 AF223487.1	NT	Homo sapiens NP0088 protein (NP0088) mRNA, complete cds		
7418	18842		1.83	3.0E-19	114922/4	NT	Homo sapiens similar to alpha-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC083222), mRNA	
8380	20319	33220	1.2	3.0E-19 X89885.1	NT	M.musculus mRNA for TPCR33 protein		
12084	24347		16.44	3.0E-19 AF165520.1	NT	Homo sapiens phorbol I protein (IPB1) mRNA, complete cds		
2595	15157	27725	7.09	2.0E-19 AL1632012	NT	Homo sapiens chromosome 21 segment HS21C001		
4542	17128		1.28	2.0E-19 AI311783.1	EST_HUMAN	#681602.x1 NCI_CGAP_K65 Homo sapiens cDNA clone IMAGE:18153888 3' similar to TR-CR883386 Q883386	POLYEN GENE ;	
8272	20813	33735	8.35	2.0E-19 AA012954.1	EST_HUMAN	#2834089.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:380880 5'		
9823	22221	35308	0.81	2.0E-19 Q85155	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN QLF2		
507	13140		1.85	1.0E-19 BE408611.1	EST_HUMAN	601304125f1 NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:38883105		